

05/05/99
JCS71 U.S. PTO
Frederick P. Fish
1855-1930
W.K. Richardson
1859-1951

FISH & RICHARDSON P.C.

A
Box Seg
225 Franklin Street
Boston, Massachusetts
02110-2804
Telephone
617 542-5070
Facsimile
617 542-8900
Web Site
www.fr.com

May 5, 1999

Attorney Docket No.: 06501/030001

Box Patent Application

Assistant Commissioner for Patents
Washington, DC 20231

Presented for filing is a new original patent application of:

Applicant: HIROAKI YAMAMOTO
Title: METHOD FOR PRODUCING OPTICALLY ACTIVE
4-HALO-3-HYDROXYBUTYRIC ACID ESTER

Enclosed are the following papers, including those required to receive a filing date under 37 CFR §1.53(b):

	<u>Pages</u>
Specification	52
Claims	4
Abstract	1
Signed Declaration [To Be Filed At A Later Date]	
Drawing(s)	4

Enclosures:

- Nucleotide and/or amino acid sequence listing including:
 - Computer readable copy.
 - Paper copy, 10 pages.
 - Verification statement, 1 page.
- A certified copy of the priority application will be filed at a later date.
- Postcard.

"EXPRESS MAIL" Mailing Label Number EL245412378US

Date of Deposit May 5, 1999

I hereby certify under 37 CFR 1.10 that this correspondence is being deposited with the United States Postal Service as "Express Mail Post Office To Addressee" with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.

Thomas McElroy

Thomas McElroy

FISH & RICHARDSON P.C.

May 5, 1999

Page 2

Under 35 USC §119, this application claims the benefit of foreign priority applications filed in Japan: serial number 10/126507, filed May 8, 1998; serial number 10/300178, filed October 21, 1998; and serial number 11/98205, filed April 5, 1999.

Basic filing fee	760.00
Total claims in excess of 20 times \$18.00	36.00
Independent claims in excess of 3 times \$78.00	0.00
Fee for multiple dependent claims	0.00
Total filing fee:	\$ 796.00

A check for the filing fee is enclosed. Please apply any other required fees or any credits to Deposit Account No. 06-1050, referencing the attorney docket number shown above.

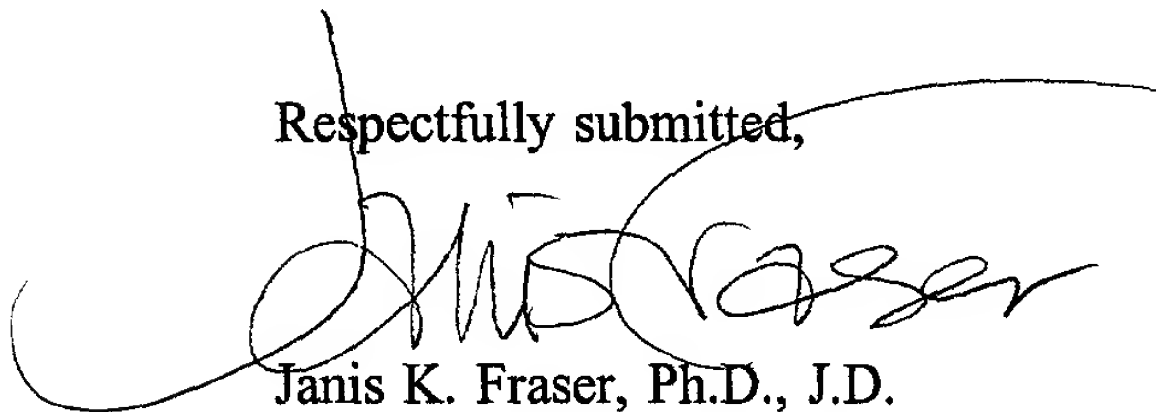
If this application is found to be incomplete, or if a telephone conference would otherwise be helpful, please call the undersigned at 617/542-5070.

Kindly acknowledge receipt of this application by returning the enclosed postcard.

Please send all correspondence to:

Janis K. Fraser, Ph.D., J.D.
Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804

Respectfully submitted,



Janis K. Fraser, Ph.D., J.D.
Reg. No. 34,819

Enclosures

371149.B11

APPLICATION
FOR
UNITED STATES LETTERS PATENT

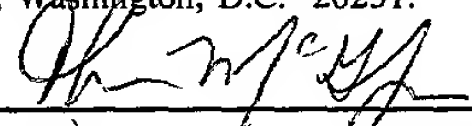
TITLE: **METHOD FOR PRODUCING OPTICALLY ACTIVE
4-HALO-3-HYDROXYBUTYRIC ACID ESTER**

APPLICANT: **HIROAKI YAMAMOTO**

"EXPRESS MAIL" Mailing Label Number EL245412378US

Date of Deposit May 5, 1999

I hereby certify under 37 CFR 1.10 that this correspondence is being deposited with the United States Postal Service as "Express Mail Post Office To Addressee" with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231.



Thomas McEllyn

METHOD FOR PRODUCING OPTICALLY ACTIVE
4-HALO-3-HYDROXYBUTYRIC ACID ESTER

FIELD OF THE INVENTION

The present invention relates to a method for preparing (S)-4-halo-3-hydroxybutyric acid ester using β -ketoacyl-acylcarrier-protein reductase comprising Type II fatty acid synthase or acetoacetyl-CoA reductase comprising poly- β -hydroxy fatty acid synthase.

BACKGROUND OF THE INVENTION

Known methods for preparing the optically active (S)-4-halo-3-hydroxybutyric acid ester include an asymmetric reduction method using 3- α -hydroxysteroid dehydrogenase (Japanese Patent Laid-Open Publication No. Hei 1-277494) and microorganisms such as baker's yeast (J. Am. Chem. Soc. 105, 5925-5926 (1983); Japanese Patent Laid-Open Publication No. Sho 61-146191). D-enzyme-1 and D-enzyme-2 have been reported as the enzyme of baker's yeast reducing 4-haloacetoacetic acid ester to produce (S)-4-halo-3-hydroxybutyric acid ester (J. Org. Chem. 56, 4778-4483 (1991)). Of these enzymes, D-enzyme-2 has been indicated to be the fatty acid synthase based on its molecular weight, etc. (J. Am. Chem. Soc. 107, 2993 (1985)).

However, in the synthesis of optically active (S)-4-halo-3-hydroxybutyric acid ester by reducing 4-haloacetoacetic acid ester using baker's yeast, the enzymatic activity is too low to produce the desired product in a high concentration. Furthermore, since baker's yeast has an enzyme reducing 4-haloacetoacetic acid ester to produce (R)-4-halo-3-hydroxybutyric acid ester, it is difficult to stably synthesize (S)-4-halo-3-hydroxybutyric acid ester with a high optical purity.

In addition, the fatty acid synthase mainly involved in the synthesis of (S)-4-halo-3-hydroxybutyric acid ester in baker's yeast has been reported to be quickly inhibited by SH reagents such as iodoacetamide, mercury, and p-(chloromercury)benzoic acid. Thus, the enzyme is expected to be inhibited by the substrate 4-haloacetoacetic acid ester and the product 4-halo-3-hydroxybutyric acid ester. Therefore, baker's yeast is not preferable for producing (S)-4-halo-3-hydroxybutyric acid ester in a large quantity.

It is also conceivable to synthesize (S)-4-halo-3-hydroxybutyric acid ester with a high optical purity by highly expressing the fatty acid synthase of baker's yeast with a high specific activity in heterologous microorganisms using genetic engineering techniques. However, the fatty acid synthase of baker's yeast is an extremely complex multicatalytic enzyme, in which α -subunit with the molecular weight of 208,000 consisting of 1,894 amino acid residues and β -subunit with the molecular weight of 229,000 consisting of 2,051 amino acid residues (J. Biol. Chem. 263, 12315-12325 (1988)) form an $\alpha_6\beta_6$ complex (J. Biol. Chem. 253, 4464-4475 (1978)), having eight different activities, besides the β -keto group reducing activity (β -ketoacyl-ACP reducing activity), including the acyl carrier protein (ACP) activity, ACP-S-acetyltransferase activity, ACP-S-malonyl transferase activity, β -ketoacyl-ACP synthase activity, β -hydroxyacyl-ACP dehydrogenase activity, enoyl-ACP reductase activity, and palmitoyl transferase activity. Therefore, it is not easy to highly express this synthase in heterologous microorganisms. For example, an attempt to express FAS1 and FAS2 in minicells of *E. coli* reportedly resulted in failure to detect a full length of the enzymes (Ann. Rev. Biochem. 52, 537-579 (1983)).

The domain for the β -ketoacyl-ACP reducing activity which is expected to exhibit the 4-haloacetoacetic acid ester reductase activity has been indicated to be located in the α -subunit of the fatty acid synthase based on the amino acid sequence. It has been reported, however, that, when the α -subunit was completely dissociated by freeze-thawing in a high salt concentration (Biochem. J. 109, 312-314 (1968)) and by lysine modification with dimethyl maleic anhydride, the subunit alone did not express the β -ketoacyl-ACP reducing activity (Eur. J. Biochem. 94, 189-197 (1979)). It has also been reported that ethyl acetoacetate reducing activity was not expressed by the fatty acid synthase with an $\alpha_6\beta_6$ structure but expressed only by that with an $\alpha_2\beta_2$ structure (Mw 800,000) (Eur. J. Biochem. 172, 633-639 (1988)). Therefore, it has not been clarified which domain of the fatty acid synthase is essential for the 4-haloacetoacetic acid reducing activity and how to efficiently prepare the structure ($\alpha_2\beta_2$) expressing the 4-haloacetoacetic acid ester reducing activity.

SUMMARY OF THE INVENTION

An objective of the present invention is to provide a method for efficiently producing (S)-4-halo-3-hydroxybutyric acid ester utilizing an enzyme constituting fatty acid synthase or that constituting the poly- β -hydroxy fatty acid biosynthetic system.

Fatty acid synthase is structurally classified into four types, IA, IB, IC, and II (Shin Seikagaku Jikken Koza (New Biochemical Experiment) 4, Shisitu (Lipids) I, p34-37). Animals including humans (Proc. Natl. Acad. Sci. USA 92, 8695 (1995)) have Type IA synthase comprising a homodimer (Mw about 500,000) of α -subunit (Mw about 250,000) having all of the above-described eight different activities

of fatty acid synthase. Yeasts including baker's yeast and fungi have Type IB synthase of an $\alpha_6\beta_6$ structure (Mw about 2,400,000) consisting of α -subunit (Mw about 210,000) and β -subunit (Mw about 200,000) expressing all the fatty acid synthase activities. Bacteria such as *Brevibacterium ammoniagenes* (Eur. J. Biochem. 247, 268 (1997)) and *Micobacterium smegmatis* (Physiol. Rev. 56, 339 (1976)) have Type IC synthase of an α_6 structure consisting of α -subunit (Mw about 250,000) having all the fatty acid synthase activities. Plants such as *Brassica napus* (Biochim. Biophys. Acta, 1120, 151 (1992)) and algae, bacteria such as *Escherichia coli*, *Actinomycetes*, and viruses have Type II synthase in which individual reactions of the fatty acid synthase are carried out with separate enzyme proteins.

Taking notice of β -ketoacyl-ACP reductase classified into Type II fatty acid synthase, among these various types of enzymes, which is simpler in the structure and functions, smaller in molecular weight (Mw of subunit about 20,000 to 40,000) as compared with Type I enzymes (IA, IB, and IC), and not inhibited by SH reagents, the present inventors have thought that, if the enzyme has the activity to reduce 4-haloacetoacetic acid ester to synthesize (S)-4-halo-3-hydroxybutyric acid ester like Type IB fatty acid synthase of baker's yeast, it would be possible to produce (S)-4-halo-3-hydroxybutyric acid ester in a large quantity and create a microbial strain capable of producing (S)-4-halo-3-hydroxybutyric acid ester in high yield utilizing genetic engineering techniques.

Therefore, the present inventors have attempted the isolation of β -ketoacyl-ACP reductase constituting Type II fatty acid synthase to investigate its reducing activity toward 4-haloacetoacetic acid ester.

Specifically, β -ketoacyl-ACP reductase genes of *Escherichia coli* or *Bacillus subtilis*, whose nucleotide sequences were known, were cloned by the polymerase chain reaction with chromosomal DNAs from respective bacteria as the template. The isolated gene was then introduced into *Escherichia coli* to highly express the enzyme therein to examine its 4-chloroacetoacetic acid ester reducing activity. As a result, the present inventors have found that the enzyme has an extremely high reducing activity and stereoselectivity toward 4-chloroacetoacetic acid ester.

In addition, while it has been reported that β -ketoacyl-ACP reductase from *Escherichia coli* showed an oxidizing activity specific to the D-stereoisomer of β -hydroxybutyl-ACP (J. Biol. Chem. 240, 618-621 (1965)), the present inventors have found that the enzyme as well as the enzyme derived from *Bacillus subtilis* showed almost no oxidizing activity to 4-chloro-3-hydroxybutyric acid ester of either configuration, but only reducing ethyl 4-chloroacetoacetate. Such a property is extremely advantageous for synthesizing an optically active (S)-4-halo-3-hydroxybutyric acid ester by asymmetric reduction because the reaction equilibrium is not rate-limiting.

Furthermore, the present inventors have found that genes encoding acetoacetyl-CoA reductase (generally designated phbB or phaB), one of the enzymes constituting the poly- β -hydroxy fatty acid (PHA) biosynthesis system, have homology to that encoding Type II fatty acid synthase (generally designated fabG), and examined whether these acetoacetyl-CoA reductases are capable of asymmetrically reducing 4-chloroacetoacetic acid ester to (S)-4-halo-3-hydroxybutyric acid ester like β -ketoacyl-ACP reductase. Specifically, the inventors

isolated the acetoacetyl-CoA reductase gene from *Ralstonia eutropha*, introduced the resulting gene to *Escherihia coli* to express it, and used the expressed acetoacetyl-CoA reductase to reduce 4-chloroacetoacetic acid ester. As a result, it has been found that the enzyme has a high reducing activity and stereoselectivity for producing (S)-4-chloro-3-hydroxybutyric acid ester.

The inventors also have found that acetoacetyl-CoA reductase, like β -ketoacyl-ACP reductase, shows almost no reactivity to either optical isomer of 4-chloro-3-hydroxybutyric acid ester, and practically functions as only the reductase, which is favorable to the synthesis of (S)-4-chloro-3-hydroxybutyric acid ester.

Furthermore, the present inventors have attempted to efficiently accelerate the reducing reaction cycle by regenerating the coenzyme (NADPH or NADH), which is consumed associated with the asymmetric reduction of 4-chloroacetoacetic acid ester in this reducing reaction system. First, the inventors introduced into *Escherihia coli* a gene encoding glucose dehydrogenase capable of regenerating the coenzyme (NADPH or NADH) and a gene encoding β -ketoacyl-ACP reductase, thereby obtaining E. coli strain capable of producing these enzymes. Then, ethyl 4-haloacetoacetate was reduced utilizing the thus-obtained transformant to measure the yield and the optical purity of ethyl (S)-chloro-3-hydroxybutyrate thus produced. As a result, it was found that the recombinant enzyme produced by the *Escherihia coli* strain has a high enzymatic activity quite suitable for producing ethyl (S)-chloro-3-hydroxybutyrate with a high optical purity.

The present invention relates to a method for producing (S)-4-halo-3-hydroxybutyric acid ester by reacting 4-halo-acetoacetic acid

ester or its derivatives with β -ketoacyl-ACP reductase constituting Type II fatty acid synthase or acetoacetyl-CoA reductase, one of the enzymes constituting the poly- β -hydroxy fatty acid biosynthesis system. More specifically, it relates to:

- (1) a method for producing (S)-4-halo-3-hydroxybutyric acid ester comprising asymmetrically reducing 4-halo-acetoacetic acid ester or its derivatives with β -ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase,
- (2) the method of (1), wherein said β -ketoacyl carrier protein reductase is derived from *Escherihia coli*,
- (3) the method of (1), wherein said β -ketoacyl carrier protein reductase is selected from the group consisting of:
 - (a) a protein comprising the amino acid sequence of SEQ ID NO: 1;
 - (b) a protein comprising a modified amino acid sequence of SEQ ID NO: 1 in which one or more amino acid residues are added, deleted, or substituted and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester; and
 - (c) a protein encoded by DNA hybridizable with the DNA comprising the nucleotide sequence of SEQ ID NO: 2 and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester,
- (4) the method of (1), wherein said β -ketoacyl-acyl carrier protein reductase is derived from microorganisms belonging to the genus *Bacillus*,
- (5) the method of (4), wherein said β -ketoacyl-acyl carrier protein reductase is derived from *Bacillus subtilis*,

(6) the method of (1), wherein said β -ketoacyl-acyl carrier protein reductase is selected from the group consisting of:

- (a) a protein comprising the amino acid sequence of SEQ ID NO: 5;
- (b) a protein comprising a modified amino acid sequence of SEQ ID NO: 5 in which one or more amino acid residues are added, deleted, or substituted and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester; and

(c) a protein encoded by DNA hybridizable with the DNA comprising the nucleotide sequence of SEQ ID NO: 6 and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester,

(7) a method for producing (S)-4-halo-3-hydroxybutyric acid ester comprising asymmetrically reducing 4-halo-acetoacetic acid ester or its derivatives with acetoacetyl-CoA reductase constituting the poly- β -hydroxy fatty acid biosynthesis system,

(8) a method of (7), wherein said acetoacetyl-CoA reductase is derived from microorganisms belonging to the genus *Ralstonia*,

(9) a method of (8), wherein said acetoacetyl-CoA reductase is derived from *Ralstonia eutropha*,

(10) the method of (7), wherein said acetoacetyl-CoA reductase is selected from the group consisting of:

- (a) a protein comprising the amino acid sequence of SEQ ID NO: 9;
- (b) a protein comprising a modified amino acid sequence of SEQ ID NO: 9 in which one or more amino acid residues are added, deleted, or substituted and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric

acid ester; and

(c) a protein encoded by DNA hybridizable with the DNA comprising the nucleotide sequence of SEQ ID NO: 10 and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester,

(11) the method of (1) or (7), wherein said 4-haloacetoacetic acid ester is 4-chloroacetoacetic acid ester,

(12) the method of (1) or (7), wherein said 4-haloacetoacetic acid ester is ethyl 4-chloroacetoacetate,

(13) the method of (1), wherein said method uses a microorganism capable of producing β -ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase and an enzyme catalyzing production of NAD(P)H from NAD(P)⁺,

(14) the method of (13), wherein said microorganism is a recombinant microorganism into which heterologous or homologous DNA encoding the β -ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase and heterologous or homologous DNA encoding an enzyme catalyzing production of NAD(P)H from NAD(P)⁺, and is capable of expressing both enzymes,

(15) the method of (14), wherein said microorganism is *Escherichia coli*,

(16) the method of any one of (13) through (15), wherein said enzyme catalyzing production of NAD(P)H from NAD(P)⁺ is glucose dehydrogenase,

(17) the method of (7), wherein said method uses a microorganism capable of producing acetoacetyl-CoA reductase constituting the poly- β -hydroxy fatty acid biosynthesis system and an enzyme catalyzing production of NAD(P)H from NAD(P)⁺,

(18) the method of (17), wherein said microorganism is a recombinant

microorganism into which heterologous or homologous DNA encoding acetoacetyl-CoA reductase constituting the poly- β -hydroxy fatty acid biosynthesis system and heterologous or homologous DNA encoding an enzyme catalyzing production of NAD(P)H from NAD(P)⁺ and capable of expressing both enzymes,

(19) the method of (18), wherein said microorganism is *Escherichia coli*, and

(20) the method of any one of (17) through (19), wherein said enzyme catalyzing production of NAD(P)H from NAD(P)⁺ is glucose dehydrogenase.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the restriction map of plasmid pSE420D. P(trc) represents the trc promoter, T(rrnB) the rrnB T1T2 terminator, Amp the β -lactamase gene for ampicillin resistance, and ori the replication origin of plasmid.

Figure 2 shows the restriction map of plasmid pSG-ECR1. P(trc) represents the trc promoter, EcfabG the β -ketoacyl ACP reductase gene derived from *Escherichia coli*, BSGlcDH the glucose dehydrogenase gene derived from *Bacillus subtilis*, T(rrnB) the rrnB T1T2 terminator, Amp the β -lactamase gene for ampicillin resistance, and ori the replication origin of plasmid.

Figure 3 shows the restriction map of plasmid pSG-BSR1. P(trc) represents the trc promoter, BcfabG the β -ketoacyl ACP reductase gene derived from *Bacillus subtilis*, BSGlcDH the glucose dehydrogenase gene derived from *Bacillus subtilis*, T(rrnB) the rrnB T1T2 terminator, Amp the β -lactamase gene for ampicillin resistance, and ori the replication origin of plasmid.

Figure 4 shows the restriction map of plasmid pSG-AER1. P(trc)

represents the trc promoter, AephbB the acetoacetyl-CoA reductase gene derived from *Ralstonia eutropha*, BSGlcDH the glucose dehydrogenase gene derived from *Bacillus subtilis*, T(rrnB) the rrnB T1T2 terminator, Amp the β -lactamase gene for ampicillin resistance, and ori the replication origin of plasmid.

DETAILED DESCRIPTION OF THE INVENTION

The method for producing (S)-4-halo-3-hydroxybutyric acid ester of the present invention uses the enzyme constituting Type II fatty acid synthase (EC1.1.1.100) or acetoacetyl-CoA reductase (EC 1.1.1.36) constituting the PHA biosynthesis system. The enzyme (EC 1.1.1.100) constituting Type II fatty acid synthase is simpler in the structure and functions, smaller in the molecular weight (Mw of subunit about 20,000 to 40,000), and not inhibited by SH reagents as compared with Type IA synthase comprising a homodimer of α -subunit, Type IB synthase of an $\alpha_6\beta_6$ structure consisting of α -subunit and β -subunit, and Type IC synthase of an α_6 structure of α -subunit, which have all of various activities of fatty acid synthase. Therefore, Type II synthase is advantageous and preferable for large quantity production of (S)-4-halo-3-hydroxybutyric acid ester and construction of a microbial strain capable of high level production of (S)-4-halo-3-hydroxybutyric acid ester.

The source of the synthase used is not particularly limited. In addition to β -ketoacyl-ACP reductase derived from *Escherichia coli* (SEQ ID NO: 1, J. Biol. Chem. 267, 5751-5754 (1992)) and that derived from *Bacillus subtilis* (SEQ ID NO: 5, J. Bacteriol. 178, 4794-4800 (1996)), and enzymes derived from other various organisms can be used. The enzymes derived from other organisms include β -ketoacyl-ACP reductase

derived from *Actinobacillus actinomycetemcomitans* (Biochem. Biophys. Res. Commun, 230, 220-225 (1997)), *Bacillus subtilis* (J. Bacteriol. 178, 4794-4800 (1996)), *Escherichia coli* (J. Biol. Chem. 267, 5751-5754 (1992)), *Mycobacterium bovis* (Science 267, 227-230 (1994)), *Mycobacterium smegmatis* (DDBJ Accession number U66800), *Mycobacterium tuberculosis* (Mol. Microbiol. 15, 1009-1015 (1995)), *Propionibacterium shermanii* (J. Gen. Microbiol. 127, 121-129 (1981)), *Streptococcus pneumoniae* (WO97/43303), *Synechocystis* sp. (DNA Res. 3, 109-136 (1996)), *Thermotoga maritima* (J. Bacteriol. 178, 248-257 (1996)), *Vibrio harveyi* (J. Bacteriol. 178, 571-573 (1996)), *Haemophilus influenza* (Science 269, 469-512 (1995)), etc. β -ketoacyl-ACP reductases derived from plants include those derived from *Allium porrum* (Plant Physiol. 115, 501-510 (1997)), *Arabidopsis thaliana* (Biochem. J. 283, 321-326 (1992), Plant Physiol. 115, 501-510 (1997)), *Brassica napus* (WO96/02652)), *Carthamus tinctorius* (Arch. Biochem. Biophys. 217, 144-154 (1982)), *Cuphea lanceolata* (Mol. Gen. Genet. 233, 122-128 (1992)), *Hordeum vulgare* (Plant Physiol. 115, 501-510 (1997)), *Persea americana* (Biochem. J. 271, 713-720 (1990)), carrot (Arch. Biochem. Biophys. 300, 157-163 (1993)), *Euglena gracilis* (J. Biol. Chem. 255, 1504-1508 (1980)), *Spinacia oleracea* (Plant Physiol. 69, 1257-1262 (1982)), *Zea mays* L. (Plant Physiol. 115, 501-510 (1997)), etc.

A gene encoding β -ketoacyl-ACP reductase can be isolated utilizing, for example, hybridization techniques. A β -ketoacyl-ACP reductase gene derived from various organisms can be isolated by hybridization, under the stringent conditions, with the DNA encoding β -ketoacyl-ACP reductase derived from *Escherichia coli* (SEQ ID NO: 2) and that from *Bacillus subtilis* (SEQ ID NO: 6), or DNAs prepared from

other organisms using the portions thereof as the probe. The polymerase chain reaction can also be utilized to isolate the desired gene. For example, primers are designed based on the highly homologous region in the gene encoding β -ketoacyl-ACP reductase (e.g. NADPH-binding region, 10th to 34th amino acid residues of β -ketoacyl-ACP reductase from *Escherichia coli*) and, using the resulting primers and the chromosomal DNA or cDNA of a target organism as the template, the polymerase chain reaction is performed to isolate the gene encoding β -ketoacyl-ACP reductase from various organisms.

Poly- β -hydroxy fatty acid (PHA) is known to accumulate in more than 100 varieties of prokaryotic microorganisms including the genus *Alcaligenes*, *Aphanotheca*, *Azotobacter*, *Bacillus*, *Pseudomonas*, *Rhodospirillum*, and *Actinomyces*. The PHA biosynthetic system comprises 3-ketothiolase, acetoacetyl CoA reductase and PHA synthase. Among them, acetoacetyl CoA reductase comprises a tetramer of the subunit with Mw 20,000 to 40,000 and preferably uses reduced nicotinamide adenine dinucleotide phosphate (NADPH) as the coenzyme for the reducing reaction. It can also employ a more economical and highly stable reduced nicotinamide adenine dinucleotide (NADH) as the coenzyme and thus is industrially advantageous.

Any acetoacetyl CoA reductases can be used in the present invention regardless of their origin so far as they are acetoacetyl CoA reductase participating in the PHA biosynthesis. Examples thereof include acetoacetyl CoA reductase derived from *Acinetobacter* sp. RA3849 (J. Bacteriol. 177, 4501-4507 (1995)), *Ralstonia eutropha* (previously called *Alcaligenes eutrophus*, FEMS Microbiol. Lett. 52, 259-264 (1988)), *Alcaligenes latus* (J. Microbiol. Biotechnol. 6, 425-431 (1996)),

Alcaligenes sp. SH-69 (DDBJ Accession No. AF002014), *Azospirillum brasilense* (J. Gen. Microbiol. 136, 1191-1196 (1990), Mol. Gen. Genet. 231, 375-384 (1992)), *Azotobacter beijerinckii* (Biochem. J., 134, 225-238 (1973)), *Bacillus megaterium* (Can. J. Microbiol. 41 (Suppl. 1), 77-79 (1995)), *Chromatium vinosum* D strain (Eur. J. Biochem. 209, 135-150 (1992)), *Ectothiorhodospira shaposhnikovii* (Appl. Microbiol. Biotechnol. 40, 292-300 (1993)), *Lupinus luteus* (Plant Soil, 56, 379-390 (1980)), *Methylobacterium extorquens* (FEMS Microbiol. Lett. 156, 275-279 (1997)), *Methylobacterium rhodesianum* MB 126 (Arch. Microbiol. 161, 277-280 (1994)), *Paracoccus denitricans* (FEMS Microbiol. Rev. 103, 257-264 (1992), FEMS Microbiol. Lett. 133, 85-90 (1995)), *Pseudomonas* sp. (DDBJ Accession No. Z80156), *Rhizobium lupini* (Fiziol. Rast. (Moscow) 27, 544-550 (1980)), *Rhizobium meliloti* 41 or *Sinorhizobium meliloti* (Microbiology, 141, 2553-2559 (1995)), *Rhodococcus ruber* NCIMB 40126 (FEMS Microbiol. Rev., 103, 93-101 (1992)), *Synechococcus* sp. (Japanese Patent Laid-open Publication No. Hei 8-187085), *Syntrophomonas wolfei* subsp. *wolfei* (Arch. Microbiol. 159, 16-20 (1993)), *Thiocapsa pfennigii* (Appl. Microbiol. Biotechnol. 40, 292-300 (1993)), and *Zoogloea ramigera* I-16-M (Arch. Microbiol. 114, 211-217 (1977), J. Biol. Chem. 262, 97-102 (1987)).

If the nucleotide sequence of the gene encoding acetoacetyl-CoA reductase is known, the coding region can be isolated using the polymerase chain reaction (PCR). The acetoacetyl-CoA reductase gene can also be isolated from various organisms by hybridizing, under the stringent conditions, the target DNA with DNA encoding acetoacetyl-CoA reductase derived from, for example, *Ralstonia eutropha* (SEQ ID NO: 10, the amino acid sequence of the enzyme is shown in SEQ ID NO: 9) or DNA

prepared from other organisms using the portions of the above enzyme-encoding DNA as the probe. Furthermore, it is also possible to isolate the acetoacetyl-CoA reductase gene from various organisms utilizing the polymerase chain reaction (PCR) with primers designed based on a highly homologous region (such as the NADPH-binding region) of the gene encoding acetoacetyl-CoA reductase and the chromosomal DNA or cDNA from a target organism as the template.

In the method of the present invention, may be used not only naturally-occurring enzymes but also variant enzymes having modified amino acid sequence of the natural enzyme so far as the variant enzymes are functionally equivalent to the natural enzyme. Such modification of the amino acid sequence can be made by the method using BAL31 exonuclease III, Kunkel method, and PCR, which are well known to those skilled in the art (Labomannual Genetic Engineering, 3rd ed., p219-230, Maruzen). Since the amino acid substitution may occur spontaneously, not only enzymes having amino acid artificially modified but also enzymes with spontaneously modified amino acid sequence can be used in the present invention.

In addition, the enzyme genes used in the method of the present invention include the gene having homology to β -ketoacyl-ACP reductase or acetoacetyl-CoA reductase and encoding Type II synthase of polyketides biosynthesized through the system similar to that of fatty acid synthesis and PHB synthesis (e.g. the open reading frame (ORF)-3 gene of the actI gene derived from *Saccharopolyspora hirsuta*, Mol. Gen. Genet. 240, 146-150 (1993)), ORF-5 in the gene having homology to the above actI gene derived from *Streptomyces cinnamonensis* and putatively participating in the biosynthesis of monensin (Mol. Gen. Genet. 234,

254-264 (1992)), actIII that is a gene for actinorhodin biosynthesis derived from *Streptomyces coelicolor* (Gene 74, 305-320 (1988)), aknA that is a gene for Aklavinone biosynthesis derived from *Streptomyces galilaeus* (J. Bacteriol., 176, 2473-2475 (1994)), dauB that is a gene for daunomyin biosynthesis derived from *Streptomyces* sp. C5 (J. Bacteriol., 176, 6270-6280 (1994)), ORF-5 of the gene for granaticin polyketide synthase putative ketoacyl reductase 1 derived from *Streptomyces violaceoruber* Tu22, ORF-6 of the gene for the granaticin polyketide synthase putative ketoacyl reductase 2 (EMBO J., 8, 2717-2725 (1989), etc.), nodG that is a gene involved in the nodulation derived from *Rhizobium meliloti* RCR2011 (Nucleic Acids Res. 14, 7453-7472 (1986)), and hetN that is a gene involved in the heterocyst formation derived from *Anabaena* sp. (PCC 7120) (J. Bacteriol. 176, 2282-2292 (1994)). These can be preferably used as long as enzymes (such as β -ketoacyl reductase), products of these genes, have the activity to reduce 4-halo-acetoacetic acid ester to produce (S)-4-halo-3-hydroxybutyric acid.

In the present invention, "asymmetric reduction of 4-halo-acetoacetic acid ester or its derivatives using β -ketoacyl-acyl carrier protein (ACP) reductase or acetoacetyl-CoA reductase" is not necessarily performed using the purified enzyme. Microorganisms and plants containing said enzyme, or their treated products can also be used. Especially, it is preferable to use organisms transformed with a heterologous or homologous gene encoding β -ketoacyl-ACP reductase or acetoacetyl-CoA reductase using genetic engineering techniques to enable high level expression of the enzyme or the treated products of the organisms. If the organism having β -ketoacyl-ACP reductase or

acetoacetyl-CoA reductase also possesses the enzyme reducing 4-halo-acetoacetic acid ester or its derivatives to synthesize (R)-4-halo-3-hydroxybutyric acid ester, such a organism is preferably mutated to delete these (R)-enatiomer generating enzymes by the natural or artificial mutation or recombinant DNA techniques.

The host microorganisms used the present invention are not particularly limited as long as they can be transformed with DNA encoding the polypeptide having the activity of β -ketoacyl-ACP reductase or acetoacetyl-CoA reductase and express these enzyme activities. Specific examples thereof include bacteria for which the host vector system has been developed, such as the genera *Escherichia*, *Bacillus*, *Pseudomonas*, *Serratia*, *Brevibacterium*, *Corynebacterium*, *Streptococcus*, and *Lactobacillus*, yeasts such as *Saccharomyces*, *Kluyveromyces*, *Schizosaccharomyces*, *Zygosaccharomyces*, *Yarrowia*, *Trichosporon*, *Rhodospiridium*, *Hansenula*, *Pichia*, and *Candida*, and fungi such as the genera *Neurospora*, *Aspergillus*, *Cephalosporium*, and *Trichoderma*.

Transformants can be prepared by techniques conventionally used in the field of molecular biology, biotechnology, and genetic engineering (e.g., Sambrook et al., Molecular Cloning, Cold Spring Harbor Laboratories). In order to express the gene for β -ketoacyl-ACP reductase or acetoacetyl-CoA reductase of the present invention in microorganisms and the like host, it is necessary to first introduce the gene into a plasmid or phage vector that can be stably present in microorganisms to transcript and translate the genetic information. For that purpose, as the unit for controlling the transcription and translation, a promoter can be incorporated upstream of the 5'-side of

the gene and a terminator downstream of the 3'-side of the gene. Any promoter and terminator can be used so far as they function in microorganisms to be used as the host. Vectors, promoters, and terminators functioning in various microorganisms are described in detail in "Biseibutugaku Kisokoza (Fundamental Microbiology), 8, Idenshikogaku (Genetic Engineering), Kyoritsu", especially those usable in yeast in Adv. Biochem. Eng. 43, 78-102 (1980) and Yeast 8, 423-488 (1992).

For example, in the genus *Escherichia*, especially in *Escherichia coli*, pBR and pUC series can be used as the plasmid vector. Examples of the promoters include those derived from *lac* (β -galactosidase), *trp* (tryptophan operon), *tac* (*lac* and *trp* fused), phage λ PL, and PR. The terminators include *trpA* terminator and *rrnB* ribosomal terminator.

In the genus *Bacillus*, the plasmid pUB110 pC194 series can be used as the vector. These vectors can be integrated into chromosomes. as the promoter and the terminator, those for *apr* (alkaline protease), *npr* (neutral protease), and *amy* (α -amylase) can be used.

In the genus *Pseudomonas*, the host-vector system has been developed in *Pseudomonas putida*, *Pseudomonas cepacia*, etc. Vectors with a broad host spectrum such as pKT240 (comprising the gene required for the autonomous replication derived from RSF1010 or the like) developed based on the plasmid TOL participating in the degradation of toluene compounds can be used. An example of the promoter and terminator that can be used is those for the lipase gene (Japanese Patent Laid-Open Publication No. Hei 5-284973).

In the genus *Brevibacterium*, especially in *Brevibacterium lactofermentum*, the plasmid vector such as pAJ43 (Gene 39, 281 (1985))

can be used. In this vector, the promoters and terminators employed in *Escherichia coli* can be used.

In the genus *Corynebacterium*, especially in *Corynebacterium glutamicum*, the plasmid vectors such as pCS11 (Japanese Patent Laid-Open Publication No. Sho 57-183799) and pCB101 (Mol. Gen. Genet. 196, 175 (1984)) can be used.

In the genus *Streptococcus*, pHV1301 (FEMS Microbiol. Lett. 26, 239 (1985)) and pGK1 (Appl. Environ. Microbiol. 50, 94 (1985)) can be used as the plasmid vector.

In the genus *Lactobacillus*, vector pAM β 1 (J. Bacteriol. 137, 614 (1979)) developed for the genus *Streptococcus* and the promoter used in *Escherichia coli* can be employed.

In the genus *Saccharomyces*, especially in *Saccharomyces cerevisiae*, the plasmid YRp series, YEp series, YCp series, and YIp series can be used. The integration vector that utilizes the homologous recombination with the ribosomal RNA present in multicopies in chromosome (EP 537456) is extremely useful because it allows to integrate muticopies of a gene and stably maintain them. The promoters and terminators that can be used in this yeast are those for ADH (alcohol dehydrogenase), GAPDH (glyceraldehyde-3-phosphate dehydrogenase), PHO (acidic phosphatase), GAL (β -galactosidase), PGK (phosphoglycerate kinase), and ENO (enolase).

In the genus *Kluyveromyces*, especially in *Kluyveromyces lactis*, examples of the vectots include the plasmid 2 μ m series derived from *Saccharomyces cerevisiae*, pKD1 series (J. Bacteriol. 145, 382-390 (1981)), plasmids derived from pKG11 concerned with the killer activity, KARS series which is the autonomous replication gene in the genus

Kluyveromyces, and the vector plasmid capable of integrating to chromosome by the homologous recombination with ribosomal RNA (EP 537456). Promoters and terminators derived from ADH, PGK, etc. can be used.

In the genus *Schizosaccharomyces*, the vectors to be used are ARS (the autonomous replication-related gene) derived from *Schizosaccharomyces pombe* and the plasmid vector containing the selection marker complementing the autotrophy derived from *Saccharomyces cerevisiae* (Mol. Cell Biol. 6, 80 (1986)). ADH promoter derived from *Schizosaccharomyces pombe* can be used (EMBO J. 6, 729 (1987)).

In the genus *Zygosaccharomyces*, the plasmid vector based on pSB3 (Nucleic Acids Res. 13, 4267 (1985)) derived from *Zygosaccharomyces rouxii* can be used. Examples of the promoters are PH05 promoter derived from *Saccharomyces cerevisiae*, GAP-Zr (glyceraldehyde-3-phosphate dehydrogenase) promoter derived from *Zygosaccharomyces rouxii* (Agri. Biol. Chem. 54, 2521 (1990)).

In the genus *Hansenula*, the host vector has been developed in *Hansenula polymorpha*. The autonomous replication-related genes HARS1 and HARS2 derived from *Hansenula polymorpha* can be used as the vector. Since they are relatively unstable, the multicopy integration to chromosome is effective (Yeast 7, 431-443 (1991)). AOX promoter (alcohol oxidase) induced by methanol and FDH (formate dehydrogenase) promoter can be used.

In the genus *Pichia*, the host-vector system has been developed in *Pichia pastoris* utilizing the genes (PARS1 and PARS2) involved in the autonomous replication for *Pichia* (Mol. Cell. Biol. 5, 3376 (1985)).

In this vector, the potent promoter such as AOX inducible by the high concentration culture and methanol can be used (Nucleic Acids Res. 15, 3859 (1987)).

In the genus *Candida*, the host-vector system has been developed in *Candida maltosa*, *Candida albicans*, *Candida tropicalis*, *Candida utilis*, *Candida boidinii*, etc (Japanese Patent Laid-Open Publication No. Hei 5-344895) . *Candida maltosa*-derived ARS has been cloned (Agri. Biol. Chem. 51, 1587 (1987)) and used to develop a vector. In *Candida utilis*, a potent promoter has been developed for the vector capable of chromosomal integration (Japanese Patent Laid-Open Publication No. Hei 8-173170).

In the genus *Aspergillus*, *Aspergillus niger*, *Aspergillus oryzae*, etc. have been most comprehensively studied among fungi. Plasmids derived from these species and vectors capable of chromosomal integration are available. Promoters for the extracellular proteases and amylases can be used (Trends in Biotechnology 7, 283-287 (1989)).

In the genus *Trichoderma*, the *Trichoderma reesei*-based host-vector system has been developed. In this vector the promoter for the extracellular cellulase gene can be used (Biotechnology 7, 596-603 (1989)).

The culturing of transformants and purification of recombinant proteins from transformants can be performed by the conventional method known to those skilled in the art.

The substrate for the enzyme in the present invention is 4-halo-acetoacetic acid ester or its derivatives such as those with a substituent at the α -position. Preferable substrates are 4-chloroacetoacetic acid ester and ethyl 4-chloroacetoacetate. The

substrate concentration used in the method of this invention ranges usually from 0.1 to 50%, preferably from 1 to 20%. The enzyme amount used ranges usually from 0.01 to 500 U/ml of the reaction mixture, preferably from 0.1 to 50 U/ml. The coenzyme (NADPH or NADH) required by the enzyme is added in the reaction system if necessary in an amount of 0.00001 to 5 equivalents, preferably 0.0001 to 1 equivalent, with respect to the amount of the substrate. A buffer solution (for example, a phosphate buffer) can be used as a solvent in the reaction system to maintain the pH. A aqueous two-phase reaction system containing 10 to 90% organic solvent such as octane, hexane, toluene, ethyl acetate, n-butyl acetate, and chloroform can also be used. The reaction temperature is usually 4 to 50°C, preferably 10 to 30°C. pH is adjusted to usually 3 to 9, preferably 4 to 8. The reaction product, (S)-4-halo-3-hydroxybutyric acid ester, can be extracted by an organic solvent capable of dissolving the product well such as ethyl acetate and octane and purified by a method such as distillation.

In the above-described reaction, NADP^+ produced from NADPH during the reducing reaction is suitably converted to NADPH (acetoacetyl-CoA reductase and β -ketoacyl reductase involved in the biosynthesis of PHA and polyketides utilize not only NADPH but also NADH). The regeneration of the coenzymes can be performed utilizing the NAD(P)^+ reducing ability (such as the glycolytic pathway) of microorganisms. The NAD(P)^+ reducing ability can be increased by supplementing the reaction system with glucose or ethanol or by adding a microorganism capable of generating NAD(P)H from NAD(P)^+ , treated products thereof, or the enzyme with such an activity. For example, NAD(P)H can be regenerated using microorganisms having glucose dehydrogenase, malate dehydrogenase,

glutamate dehydrogenase, formate dehydrogenase, alcohol dehydrogenase, amino acid dehydrogenase, and/or glycerol dehydrogenase, treated products thereof, or the purified enzymes. Furthermore, the microorganism capable of producing β -ketoacyl reductase or acetoacetyl-CoA reductase can be genetically engineered to highly express these enzymes with the NAD(P)H regenerating activity, and the resulting transformant or the treated product thereof can be used in the method of the present invention.

In the present invention, it is also possible to use microorganisms capable of producing both acetoacetyl-CoA reductase and the NAD(P)H regenerating enzyme or both β -ketoacyl reductase and the NAD(P)H regenerating enzyme, or the treated products thereof. Such microorganisms can further genetically engineered to highly express these enzymes and the resulting microorganisms or their treated products can be used in the method of the present invention.

In the method of producing (S)-4-halo-3-hydroxybutyric acid ester using the microorganism capable of producing both acetoacetyl-CoA reductase and the NAD(P)H regenerating enzyme or both β -ketoacyl reductase and the NAD(P)H regenerating enzyme, or the treated products thereof, 1/50 to 1/20 volume, preferably 1/10 to 1/5 volume, based on the reaction mixture, of the culture, microbial cells recovered from the culture, or treated products thereof can be used. NAD^+ or NADP^+ can be added to the reaction mixture if necessary in an amount of 0.00001 to 5 equivalents, preferably 0.0001 to 1 equivalent, with respect to the amount of the substrate.

The reaction can also be performed using a bioreactor in which the microorganism producing the two enzymes or treated products thereof

is immobilized on κ -carrageenan, acrylamide, polyurethane, chitin, or the like carrier. The reaction using the bioreactor can be performed by continuously supplying 4-halo-acetoacetic acid ester as the substrate, the substrate for regenerating the coenzyme (e.g. glucose when glucose dehydrogenase is used as the enzyme for regenerating the coenzyme), and if required, a buffer for controlling pH, and NAD^+ or NADP^+ as the coenzyme, or repeatedly using the reaction mixture.

The present invention provides a method of producing the optically active (S)-4-halo-3-hydroxybutyric acid ester using β -ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase or acetoacetyl-CoA reductase constituting the poly- β -hydroxy fatty acid biosynthesizing system. β -Ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase is especially advantageous for constructing a highly productive system using genetic recombination techniques, enabling a more efficient production of the optically active (S)-4-halo-3-hydroxybutyric acid ester as compared with the prior art techniques.

The present invention will be described in more detail with reference to examples, but is not construed to be limited to these examples.

EXAMPLE 1

Isolation of β -ketoacyl-ACP Reductase Gene from *Escherichia coli*

Escherichia coli JM109 strain was cultured in the LB medium (containing Bacto-Tryptone 10 g, Bacto-Yeast extract 5 g, and NaCl 10 g/l) and the chromosomal DNA was prepared from the bacteria thus obtained using a Qiagen Genomic-tip (Qiagen). For the PCR cloning of the β -ketoacyl-ACP reductase gene (fabG) (J. Biol. Chem. 267, 5751-5754

(1992)) of *Escherichia coli*, the primers ECR-ATG1 (5'-AAAGGATCCAACAATGAATTTTGAAGGAAAAATCGC-3', SEQ ID NO: 3) and ECR-TAG1 (5'-TGCCTCGAGTTATCAGACCATGTACATCCCGC-3', SEQ ID NO: 4) were synthesized based on the nucleotide sequences at the 5'- and 3'-ends of the structural gene. Using the chromosomal DNA of *Escherichia coli* as the template, and the ECR-ATG1 and ECR-TAG1 primers, 30 cycles of PCR (95°C for 30 sec, 50°C for 1 min, and 75°C for 2 min) were performed to obtain the amplified DNA fragments.

The resulting DNA fragments were digested with restriction enzymes BamHI and XhoI. The plasmid vector pSE420 (Invitrogen) was digested with NcoI and BamHI, treated with the Klenow fragment, and subjected to the self-cyclization reaction to obtain the plasmid pSE420B. This pSE420B was digested with BamHI and XhoI, and ligated to the above PCR amplified fragments digested with the same two restriction enzymes using T4 DNA ligase to obtain the plasmid pSE-ECR1. The DNA insert in the plasmid thus obtained were sequenced and identified as the *fabG* gene. The nucleotide sequence of *fabG* is shown in SEQ ID NO: 2 and the amino acid sequence of the protein encoded by the gene in SEQ ID NO: 1.

EXAMPLE 2

Expression of β -ketoacyl-ACP Reductase Gene from *Escherichia coli*

Escherichia coli HB101 strain was transformed with pSE-ECR1 and the resulting transformant (*E. coli* HB101 (pSE-ECR1)) was cultured in the LB medium (5 ml) containing ampicillin (50 mg/ml) overnight. IPTG was added to the medium to 0.1 mM and the culture was further incubated for 5 h. Bacterial cells thus obtained were collected, disrupted with a Minibeatbeater 8 (BIOSPEC), and centrifuged to obtain the supernatant as the cell-free extract.

EXAMPLE 3

Reducing Activity of β -Ketoacyl-ACP Reductase from *Escherichia coli*

The reducing activity of the cell-free extract obtained in Example 2 was assayed using ethyl 4-chloroacetoacetate, ethyl acetoacetate, and acetoacetyl-CoA as the substrate.

A reaction mixture containing 50 mM potassium phosphate buffer (pH 6.5), 0.2 mM NADPH, and 20 mM the substrate (0.2 mM when acetoacetyl-CoA was used as the substrate) and the enzyme was allowed to react at 25°C. One unit of the enzyme was defined as the amount of the enzyme catalyzing the decrease of 1 μ mol of NADPH for 1 min. The results are shown in Table 1. In this table, ECAA represents ethyl 4-chloroacetoacetate, EAA ethyl acetoacetate, and AASCoA acetoacetyl-CoA, R the reducing activity, and DH the dehydrogenase activity.

Table 1

	NADPH- ECAA-R	NADPH- AASCoA-R	NADPH- EAA-R	NADP ⁺ -R- ECHB-DH	NADP ⁺ -S- ECHB-DH
Cell- free extract	100%	116%	1.90%	0.010%	0.004%

The cell-free extract expressing β -ketoacyl-ACP reductase showed the NADPH-dependent ethyl 4-chloroacetoacetate-reducing activity, and its specific activity was 0.90 U/mg protein. In contrast, the HB101 strain containing no plasmid pSE-ECR1 showed almost no ethyl 4-chloroacetoacetate-reducing activity. The extract showed approximately the same activity for acetoacetyl-CoA as that for ethyl

4-chloroacetoacetate, while almost no activity for ethyl acetoacetate having no chlorine group.

EXAMPLE 4

Oxidizing Activity of β -Ketoacyl-ACP Reductase derived from *Escherichia coli*

The oxidizing activity of the cell-free extract obtained in Example 2 was assayed using ethyl (S)- or (R)-4-chloro-3-hydroxybutyrate as the substrate. The oxidizing reaction was performed by incubating a reaction mixture containing 50 mM Tris-HCl buffer (pH 9.0), 2.5 mM NADP⁺, 20 mM the substrate, and the enzyme at 25°C. One unit of enzyme was defined as the amount of enzyme catalyzing the increase of 1 μ mol of NADPH for min. The results are shown in Table 1. As shown in Table 1, the extract showed almost no oxidizing activity for either substrate. In this table, ECHB represents ethyl 4-chloro-3-hydroxybutyrate.

EXAMPLE 5

Stereoselectivity of β -Ketoacyl-ACP Reductase derived from *Escherichia coli* for Ethyl 4-chloro-3-hydroxybutyrate

A reaction mixture (1 ml) containing 200 mM potassium phosphate buffer (pH 6.5), 146 mM NADPH, 2% ethyl 4-chloroacetoacetate (122 mM), and β -ketoacyl-ACP reductase (2 U) prepared in Example 2 was incubated at 20°C overnight. Aliquot of the reaction solution was diluted 2-fold with 0.1 N HCl and ethyl 4-chloro-3-hydroxybutyrate contained in the dilution was determined by gas chromatography. Gas chromatography was performed with a Thermon 3000 chromosolve W (2 m, Shinwakako) under the conditions of the column temperature of 150°C and the detection temperature of 250°C using a flame ionization detector (FID). As a result, the concentration of ethyl 4-chloro-3-hydroxybutyrate was found

to be 13.3 g/l with a yield of 66.3%.

Optical purity was assayed by extracting ethyl 4-chloro-3-hydroxybutyrate from the reaction mixture with ethyl acetate, removing the solvent, and subjecting the residue to the high-performance liquid chromatography using an optical resolution column (column, chiracel OD (Daicel Chemical)); mobile phase, n-hexane/isopropanol (9/2); RI detection; flow rate, 0.5 ml/min). As a result, the optical purity was 96.5% ee (S) or more.

EXAMPLE 6

Synthesis of Ethyl 4-chloro-3-hydroxybutyrate by β -ketoacyl-ACP

Reductase derived from *Escherichia coli*

A reaction solution (1 ml) containing 200 mM potassium phosphate buffer solution (pH 6.5), 2% ethyl 4-chloro-acetoacetate (122 mM), 1.0 mM NADPH, β -ketoacyl-ACP reductase (1 U), 250 mM glucose, and glucose dehydrogenase (Wako Pure Chemical) (10 U) was incubated at 25°C for 16 h. Analysis was performed in the same manner as in Example 5, indicating that ethyl 4-chloro-3-hydroxybutyrate with the optical purity of 95.4% ee (S) or more was synthesized in a yield of 98.4%.

EXAMPLE 7

Isolation of β -ketoacyl-ACP Reductase gene

from *Bacillus subtilis*

Bacillus subtilis BGSC 1A1 strain was cultured in the LB medium (containing Bacto-Tryptone 10g, Bacto-Yeast extract 5 g, and NaCl 10 g/l), and the chromosomal DNA was prepared from the microbial cells thus obtained using a Qiagen Genomic-tip (Qiagen). For the PCR cloning of the β -ketoacyl-ACP reductase gene (fabG) of *Bacillus subtilis*, the primers BSR-ATG1 (5'-GGACCATGGATATGCTTAATGATAAAACGGCTA-3', SEQ ID NO:

7) and BSR-TAA1 (5'-GAGAAGCTTCTCGAGTTACATCACCATTCCGCCG-3', SEQ ID NO: 8) were synthesized based on the sequences at the 5'- and 3'-ends of the structural gene. Using the chromosomal DNA of *Bacillus subtilis* as the template and the BSR-ATG1 and BSR-TAA1 primers, 30 cycles of PCR (95°C for 30 sec, 50°C for 1 min, and 75°C for 2 min) were performed to obtain the amplified DNA fragments.

The DNA fragments thus obtained were digested with NcoI and HindIII. The plasmid vector pSE420 (Invitrogen) was digested with NcoI and HindIII, and linked to the above PCR-amplified fragments digested with the same two restriction enzymes using T4 DNA ligase to obtain the plasmid pSE-BSR1. The DNA inserts in the plasmid thus obtained were sequenced, identifying them to be the *fabG* gene except for one amino acid substitution. Namely, GCT corresponding to Ala at the position 25 according to the database (DDBJ (DNA Data Bank of Japan, Accession No. U59433) was replaced by GAT encoding Asp at the position 25. The nucleotide sequence of the *fabG* gene thus obtained is shown in SEQ ID NO: 6, the amino acid sequence of the protein encoded by the gene in SEQ ID NO: 5.

EXAMPLE 8

Expression of β -ketoacyl-ACP Reductase Gene derived from *Bacillus subtilis*

Escherichia coli HB101 strain was transformed with pSE-BSR1 and the resulting transformant (*E. coli* HB101 (pSE-BSR1)) was cultured in the LB medium (7 ml) containing ampicillin (50 mg/ml) overnight. IPTG was added to the medium to 0.1 mM and the culture was further incubated for 5 h. Bacterial cells thus obtained were collected, disrupted with a Minibeatbeater 8 (BIOSPEC), and centrifuged to obtain the supernatant

as the cell-free extract.

EXAMPLE 9

Reducing Activity of β -Ketoacyl-ACP Reductase
derived from *Bacillus subtilis*

The reducing activity of the cell-free extract obtained in Example 8 was assayed using ethyl 4-chloroacetoacetate and acetoacetyl-CoA as the substrate in the same manner as in Example 3.

The results are shown in Table 2. In this table, ECAA represents ethyl 4-chloroacetoacetate and AASCoA acetoacetyl-CoA.

Table 2

Substrate	ECAA		AASCoA	S-ECHB	R-ECHB
	NADPH	NADH	NADPH	NADP ⁺	NADP ⁺
U/mg	0.133	0	0.030	0.002	0.002
Relative activity	100%	0.0%	22.3%	1.3%	1.3%

The cell-free extract expressing β -ketoacyl-ACP reductase showed the NADPH-dependent ethyl 4-chloroacetoacetate-reduce activity and its specific activity was 0.133 U/mg protein. In contrast, the HB101 strain containing no plasmid pSE-BSR1 showed almost no ethyl 4-chloroacetoacetate-reducing activity. The acetoacetyl-CoA-reducing activity was as low as about 22% of ethyl 4-chloroacetoacetate-reducing activity, revealing the difference from the enzyme derived from *Escherichia coli*.

EXAMPLE 10

Oxidizing Activity of β -Ketoacyl-ACP Reductase
derived from *Bacillus subtilis*

The oxidizing activity of the cell-free extract obtained in Example 8 was assayed using ethyl (S)- or (R)-4-chloro-3-hydroxybutyrate as the substrate in the same manner as in Example 4. The results are shown in Table 2. The cell extract showed almost no activity for either substrate. In table 2, ECHB represents ethyl 4-chloro-3-hydroxybutyrate.

EXAMPLE 11

Stereoselectivity of β -ketoacyl-ACP Reductase derived from *Bacillus subtilis*

A reaction mixture (1 ml) containing 200 mM potassium phosphate buffer (pH 6.5), 1 mM NADP⁺, 2% ethyl 4-chloroacetoacetate (122 mM), β -ketoacyl-ACP reductase (0.8 U) prepared in Example 8, 250 mM glucose, and glucose dehydrogenase (3.2 U) (Wako Pure Chemical) was incubated at 25°C for one day. Analysis was performed by the method according to Example 5, indicating that ethyl 4-chloro-3-hydroxybutyrate was quantitatively synthesized with the optical purity of 98.1% ee (S) or more.

EXAMPLE 12

Isolation of Acetoacetyl-CoA Reductase Gene from *Ralstonia eutropha*

Ralstonia eutropha DSM 531 was cultured in a bouillon medium (containing beef extracts 5.0 g, peptone 15.0 g, NaCl 5.0 g, and K₂HPO₄ 5.0 g/l) and the chromosomal DNA was prepared from the microbial cells thus obtained using a Qiagen Genomic-tip (Qiagen).

For the PCR cloning of the acetoacetyl-CoA reductase gene (phbB) of *Ralstonia eutropha*, the primers AER-ATG1 (5'-AGTGGATCCAATGACTCAGCGCATTGCGTA-3', SEQ ID NO: 11) and AER-TAA1 (5'-AACAAGCTTCTCGAGTTAGCCCATATGCAGGCCGC-3', SEQ ID NO: 12) were

synthesized based on the sequences at the 5'- and 3'-ends of the structural gene.

Using the chromosomal DNA of *Ralstonia eutropha* as the template and the AER-ATG1 and AER-TAA1 primers, 30 cycles of PCR (95°C for 30 sec, 50°C for 1 min and 75°C for 2 min) were performed to obtain the amplified DNA fragments.

The thus-obtained DNA fragments were digested with BamHI and HindIII. The plasmid vector pSE420 prepared by the method of Example 1 was digested with BamHI and HindIII and the digestion product was ligated to the above PCR-amplified fragments digested with the same two restriction enzymes using T4 DNA ligase to obtain the plasmid pSE-AER1.

The DNA insert in the plasmid thus obtained were sequenced and identified as the phbB gene.

EXAMPLE 13

Expression of Acetoacetyl-CoA Reductase Gene derived from *Ralstonia eutropha*

Escherichia coli HB101 strain was transformed with pSE-AER1 and the resulting transformant (*E. coli* HB101 (pSE-AER1)) was cultured in the LB medium (7 ml) containing ampicillin (50 mg/ml) overnight. IPTG was added to the medium to 0.1 mM and the culture was further incubated for 5 h.

Bacterial cells thus obtained were collected, disrupted with a Minibeatbeater 8 (BIOSPEC Inc.), and centrifuged to obtain the supernatant as the cell-free extract.

EXAMPLE 14

Reducing Activity of Acetoacetyl-CoA Reductase derived from *Ralstonia eutropha*

The reducing activity of the cell-free extract obtained in Example 13 was assayed using ethyl 4-chloroacetoacetate and acetoacetyl-CoA as the substrate by the method according to Example 3. The results are shown in Table 3.

Table 3

Substrate Coenzyme	AASCoA	ECAA		S-ECHB	R-ECHB
	NADPH	NADPH	NADH	NADP ⁺	NADP ⁺
U/mg	0.984	2.50	0.056	0	0
Relative activity	100%	255%	5.7%	0%	0%

The cell-free extract expressing acetoacetyl-CoA reductase showed the NADPH-dependent ethyl 4-chloroacetoacetate-reducing activity and its specific activity was 2.50 U/mg protein. In contrast, the HB101 strain containing no plasmid pSE-AER1 showed almost no ethyl 4-chloroacetoacetate-reducing activity.

The reducing activity with acetoacetyl-CoA was as low as about 39% of that with ethyl 4-chloroacetoacetate.

EXAMPLE 15

Oxidizing Activity of Acetoacetyl-CoA Reductase

derived from *Ralstonia eutropha*

The oxidizing activity of the cell-free extract obtained in Example 13 was assayed using ethyl (S)- or (R)-4-chloro-3-hydroxybutyrate as the substrate in the same manner as in Example 4. The results are shown in Table 3. The cell extract showed almost no oxidizing activity for either substrate.

EXAMPLE 16

Stereoselectivity of Acetoacetyl-CoA Reductase from *Ralstonia eutropha*

A reaction mixture (1 ml) containing 100 mM potassium phosphate buffer (pH 6.5), 1 mM NADP⁺, 2% (122 mM) ethyl 4-chloroacetoacetate, acetoacetyl-CoA reductase (1 U) prepared in Example 13, 243 mM glucose, and glucose dehydrogenase (2.8 U) (Wako Pure Chemical) was incubated at 25°C overnight. Analysis was performed by the method according to Example 5, revealing a synthesis of ethyl 4-chloro-3-hydroxybutyrate with the optical purity of 99% ee (S) or more in a yield of 67%.

EXAMPLE 17

Construction of the Coexpression Plasmid pSE420D

The plasmid pSE420B constructed in Example 1 was digested with MunI and SpeI and ligated with the annealing product of the synthetic DNA SE420D-S (SEQ ID NO 13: AATTCTCGAGTAATCTAGAGGAATTCTAAAA) and the synthetic DNA SE420D-A (SEQ ID NO 14: CTAGTTTTAGAATTCCTCTAGATTACTCGAG) using T4 DNA ligase to obtain the plasmid pSE420D. The restriction map of pSE420D is shown in Figure 1.

EXAMPLE 18

Cloning of Glucose Dehydrogenase Gene derived from *Bacillus subtilis*

In order to regenerate the reduced nicotinamide adenine dinucleotide phosphate, the glucose dehydrogenase gene derived from *Bacillus subtilis* (J. Bacteriol. 166, 238-243 (1986)) was cloned.

For the PCR cloning of only the open reading frame portion of the glucose dehydrogenase gene based on the nucleotide sequence described in the literature, the primers BSG-ATG1 (SEQ ID NO 15: GAGGAATTCATACATGTATCCAGATTTAAAAGGAA) and BSG-TAA2 (SEQ ID NO 16: GGTAAGCTTTCATTAACCGCGGCCTGCCTG) were synthesized based on the

sequences at the 5'- and 3'-ends of the structural gene.

Using the chromosomal DNA of *Bacillus subtilis* prepared in Example 7 as the template and the BSG-ATG1 and BSG-TAA2 primers, 30 cycles of PCR (95°C for 30 sec, 50°C for 1 min, and 75°C for 3 min and 15 sec) were performed, obtaining the amplified DNA fragments.

The thus-obtained DNA fragments were digested with EcoRI and HindIII and the digestion product was ligated with the plasmid vector pSE420L constructed in Example 17 digested with the same two restriction enzymes using T4 DNA ligase to obtain the plasmid pSE-BSG1.

Analysis of the nucleotide sequence of the DNA insert resulted in the perfect coincidence with that listed in the database (DDBJ Accession No. M12276).

The nucleotide sequence of the glucose dehydrogenase gene thus obtained is shown in SEQ ID NO: 17 and the amino acid sequence of the protein encoded by the gene in SEQ ID NO: 18.

EXAMPLE 19

Construction of the plasmid pSG-ECR1 coexpressing the β -ketoacyl-ACP Reductase Gene derived from *Escherichia coli* and the Glucose Dehydrogenase Gene derived from *Bacillus subtilis*

The plasmid pSE-ECR1 constructed in Example 1 was digested with BamHI and XhoI to obtain the DNA fragment containing the β -ketoacyl-ACP reductase gene derived from *Escherichia coli*.

The plasmid pSE-BSG1 containing the glucose dehydrogenase gene derived from *Bacillus subtilis* constructed in Example 17 was digested with BamHI and XhoI, ligated to the above DNA fragment containing the β -ketoacyl-ACP reductase gene derived from *Escherichia coli* using T4 DNA ligase to obtain the plasmid pSE-ECR1 capable of coexpressing

glucose dehydrogenase and β -ketoacyl-ACP reductase. The restriction map of the plasmid pSE-ECR1 is shown in Figure 2.

EXAMPLE 20

Construction of the plasmid pSG-ECR1 coexpressing the β -ketoacyl-ACP Reductase Gene derived from *Bacillus subtilis* and the Glucose Dehydrogenase Gene derived from *Bacillus subtilis*

The plasmid pSE-ECR1 constructed in Example 7 was digested with NcoI and XhoI to obtain the DNA fragment containing the β -ketoacyl-ACP reductase gene derived from *Bacillus subtilis*.

The plasmid pSE-BSG1 containing the glucose dehydrogenase gene derived from *Bacillus subtilis* constructed in Example 17 was digested with BamHI and XhoI, ligated to the above DNA fragment containing the β -ketoacyl-ACP reductase gene derived from *Bacillus subtilis* using T4 DNA ligase to obtain the plasmid pSG-BSR1 capable of coexpressing glucose dehydrogenase and β -ketoacyl-ACP reductase. The restriction map of the plasmid pSG-BSR1 is shown in Figure 3.

EXAMPLE 21

Construction of Plasmid pSG-AER1 coexpressing the Acetoacetyl-CoA Reductase Gene derived from *Ralstonia eutropha* and the Glucose Dehydrogenase Gene derived from *Bacillus subtilis*

The plasmid pSE-AER1 constructed in Example 12 was digested with BamHI and XhoI to obtain the DNA fragment containing the acetoacetyl-CoA reductase gene derived from *Ralstonia eutropha*.

The plasmid pSE-BSG1 containing the glucose dehydrogenase gene derived from *Bacillus subtilis* constructed in Example 17 was digested with NcoI and XhoI, ligated to the above DNA fragment containing the acetoacetyl-CoA reductase gene derived from *Ralstonia eutropha* using

T4 DNA ligase to obtain the plasmid pSG-AER1 capable of coexpressing glucose dehydrogenase and acetoacetyl-CoA reductase. The restriction map of the plasmid pSG-AER1 is shown in Figure 4.

EXAMPLE 22

Coexpression of Glucose Dehydrogenase derived from *Bacillus subtilis* and β -ketoacyl-ACP Reductase derived from *Escherichia coli* or β -ketoacyl-ACP Reductase derived from *Bacillus subtilis* or Acetoacetyl-CoA Reductase derived from *Ralstonia eutropha*

Escherichia coli HB101 strain was transformed with the plasmids pSG-ECR1, pSG-BSR1, or pSG-AER1 to coexpress glucose dehydrogenase derived from *Bacillus subtilis* with β -ketoacyl-ACP reductase derived from *Escherichia coli* or with β -ketoacyl-ACP reductase derived from *Bacillus subtilis* or with acetoacetyl-CoA reductase derived from *Ralstonia eutropha*.

Recombinant *Escherichia coli* transformed with each plasmid was inoculated to the 2xYT medium (containing Bacto-Tryptone 20 g, Bacto-Yeast extract 10 g, and NaCl 10 g/l), cultured at 30°C overnight. Adding 0.1 mM IPTG to the medium, the culturing was further performed for 4 h.

Three kinds of *Escherichia coli* transformants thus obtained were collected and subjected to the enzyme activity assay and the reducing reaction of ethyl 4-chloroacetoacetate.

EXAMPLE 23

Enzymatic Activity of *Escherichia coli* cells transformed with pSG-ECR1, pSG-BSR1 and pSG-AER1

Escherichia coli cells (corresponding to 2 ml of the culture) transformed with pSG-ECR1, pSG-BSR1, or pSG-AER1 prepared in Example

21 were separately suspended in 0.25 ml of a cell disrupting solution (containing 100 mM potassium phosphate buffer (pH 6.5), 0.02% 2-mercaptoethanol, and 0.5 M sodium chloride). The resulting solution was treated in a close ultrasonicator UCD-200TM (Cosmobio) for 3 min to disrupt the cells. The sonicated cell suspension was centrifuged and the supernatant was collected as the crude enzyme solution, which was subjected to the enzyme activity assay.

The ethyl 4-chloroacetoacetate-reducing activity was assayed in the same manner as in Example 3.

Glucose dehydrogenase activity was assayed in a reaction solution containing 100 mM potassium phosphate bufferr (pH 6.5), 2.5 mM NAD⁺, 100 mM D-glucose, and the enzyme at 25°C.

One unit of each enzyme was defined as the amount of the enzyme catalyzing the formation of 1 µmol NADH per min under the above-described reaction conditions.

Each enzyme activity and SECHB productivity of the crude enzyme solution obtained from recombinant *E. coli* containing pSG-ECR1, pSG-BSR1, or pSG-AER1 are shown in Table 4.

Table 4

Plasmid	Enzyme activity (U/ml-br)		SECHB synthesis	
	GlcDH	ECAA-R	(g/l)	ee(%)S
pSG-ECR1	0.476	0.151	20.3	93.7
pSG-BSR1	4.089	0.203	42.3	98.0
pSG-AER1	3.717	1.475	42.8	99.3

U/ml-br: enzyme activity per ml of the culture

GlcDH: glucose dehydrogenase

ECAA-R: ethyl 4-chloroacetoacetate reductase

SECHB: ethyl (S)-4-chloro-3-hydroxybutyrate

E. coli cells with no plasmid have neither glucose dehydrogenase activity nor ethyl 4-chloroacetoacetate reductase activity, while recombinant *E. coli* cells with pSG-ECR1, pSG-BSR1, or pSG-AER1 showed both enzymatic activities, indicating expression of the two enzyme genes introduced in the plasmids.

EXAMPLE 24

Synthesis of Ethyl (S)-4-chloro-3-hydroxybutyrate using *Escherichia coli* transformed with pSG-ECR1, pSG-BSR1, or pSG-AER1

Ethyl 4-chloroacetoacetate was reduced using *Escherichia coli* containing pSG-ECR1, pSG-BSR1, or pSG-AER1 prepared in Example 21.

A reaction solution (20 ml) containing each *Escherichia coli* cell prepared from 20 ml of the culture, 200 mM potassium phosphate buffer (pH 6.5), 4% ethyl 4-chloroacetoacetate, 486 mM D-glucose, and 1 mM NADP⁺ was incubated at 25°C under stirring overnight.

The amount and the optical purity of ethyl (S)-4-chloro-3-hydroxybutyrate were determined in the same manner as in Example 5. The results are shown in Table 4. As shown in Table 4, all of the three kinds of the *E. coli* transformants could produce (S)-4-chloro-3-hydroxybutyrate efficiently with high stereoselectivity.

SEQUENCE LISTING

<110> DAICEL CHEMICAL INDUSTRIES, LTD.

<120> Method for producing optically active
4-halo-3-hydroxybutyric acid ester

<130> D1-003DP2

<150> JP 1998-126507

<151> 1998-05-08

<150> JP 1998-300178

<151> 1998-10-21

<160> 12

<170> PatentIn Ver. 2.0

<210> 1

<211> 244

<212> PRT

<213> Escherichia coli

<400> 1

Met Asn Phe Glu Gly Lys Ile Ala Leu Val Thr Gly Ala Ser Arg Gly
1 5 10 15

Ile Gly Arg Ala Ile Ala Glu Thr Leu Ala Ala Arg Gly Ala Lys Val
20 25 30

Ile Gly Thr Ala Thr Ser Glu Asn Gly Ala Gln Ala Ile Ser Asp Tyr
35 40 45

Leu Gly Ala Asn Gly Lys Gly Leu Met Leu Asn Val Thr Asp Pro Ala
50 55 60

Ser Ile Glu Ser Val Leu Glu Lys Ile Arg Ala Glu Phe Gly Glu Val
65 70 75 80

Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Asn Leu Leu Met
85 90 95

Arg Met Lys Asp Glu Glu Trp Asn Asp Ile Ile Glu Thr Asn Leu Ser
100 105 110

Ser Val Phe Arg Leu Ser Lys Ala Val Met Arg Ala Met Met Lys Lys
115 120 125

Arg His Gly Arg Ile Ile Thr Ile Gly Ser Val Val Gly Thr Met Gly
130 135 140

Asn Gly Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala Gly Leu Ile Gly
145 150 155 160

Phe Ser Lys Ser Leu Ala Arg Glu Val Ala Ser Arg Gly Ile Thr Val
165 170 175

Asn Val Val Ala Pro Gly Phe Ile Glu Thr Asp Met Thr Arg Ala Leu
180 185 190

Ser Asp Asp Gln Arg Ala Gly Ile Leu Ala Gln Val Pro Ala Gly Arg
195 200 205

Leu Gly Gly Ala Gln Glu Ile Ala Asn Ala Val Ala Phe Leu Ala Ser
210 215 220

Asp Glu Ala Ala Tyr Ile Thr Gly Glu Thr Leu His Val Asn Gly Gly
225 230 235 240

Met Tyr Met Val

<210> 2

<211> 735

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(735)

<400> 2

atg aat ttt gaa gga aaa atc gca ctg gta acc ggt gca agc cgc gga 48
Met Asn Phe Glu Gly Lys Ile Ala Leu Val Thr Gly Ala Ser Arg Gly
1 5 10 15

att ggc cgc gca att gct gaa acg ctc gca gcc cgt ggc gcg aaa gtt 96
Ile Gly Arg Ala Ile Ala Glu Thr Leu Ala Ala Arg Gly Ala Lys Val
20 25 30

att ggc act gcg acc agt gaa aat ggc gct cag gcg atc agt gat tat 144
Ile Gly Thr Ala Thr Ser Glu Asn Gly Ala Gln Ala Ile Ser Asp Tyr
35 40 45

tta ggt gcc aac ggc aaa ggt ctg atg ttg aat gtg acc gac ccg gca 192
Leu Gly Ala Asn Gly Lys Gly Leu Met Leu Asn Val Thr Asp Pro Ala
50 55 60

tct atc gaa tct gtt ctg gaa aaa att cgc gca gaa ttt ggt gaa gtg 240
Ser Ile Glu Ser Val Leu Glu Lys Ile Arg Ala Glu Phe Gly Glu Val
65 70 75 80

CCDS:CCDS_10000.1

gat atc ctg gtc aat aat gcc ggt atc act cgt gat aac ctg tta atg	288
Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Asn Leu Leu Met	
85 90 95	
cga atg aaa gat gaa gag tgg aac gat att atc gaa acc aac ctt tca	336
Arg Met Lys Asp Glu Glu Trp Asn Asp Ile Ile Glu Thr Asn Leu Ser	
100 105 110	
tct gtt ttc cgt ctg tca aaa gcg gta atg cgc gct atg atg aaa aag	384
Ser Val Phe Arg Leu Ser Lys Ala Val Met Arg Ala Met Met Lys Lys	
115 120 125	
cgt cat ggt cgt att atc act atc ggt tct gtg gtt ggt acc atg gga	432
Arg His Gly Arg Ile Ile Thr Ile Gly Ser Val Val Gly Thr Met Gly	
130 135 140	
aat ggc ggt cag gcc aac tac gct gcg gcg aaa gcg ggc ttg atc ggc	480
Asn Gly Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala Gly Leu Ile Gly	
145 150 155 160	
ttc agt aaa tca ctg gcg cgc gaa gtt gcg tca cgc ggt att act gta	528
Phe Ser Lys Ser Leu Ala Arg Glu Val Ala Ser Arg Gly Ile Thr Val	
165 170 175	
aac gtt gtt gct ccg ggc ttt att gaa acg gac atg aca cgt gcg ctg	576
Asn Val Val Ala Pro Gly Phe Ile Glu Thr Asp Met Thr Arg Ala Leu	
180 185 190	
agc gat gac cag cgt gcg ggt atc ctg gcg cag gtt cct gcg ggt cgc	624
Ser Asp Asp Gln Arg Ala Gly Ile Leu Ala Gln Val Pro Ala Gly Arg	
195 200 205	
ctc ggc ggc gca cag gaa atc gcc aac gcg gtt gca ttc ctg gca tcc	672
Leu Gly Gly Ala Gln Glu Ile Ala Asn Ala Val Ala Phe Leu Ala Ser	
210 215 220	
gac gaa gca gct tac atc acg ggt gaa act ttg cat gtg aac ggc ggg	720
Asp Glu Ala Ala Tyr Ile Thr Gly Glu Thr Leu His Val Asn Gly Gly	
225 230 235 240	
atg tac atg gtc tga	735
Met Tyr Met Val	

<210> 3

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 3
aaaggatcca acaatgaatt ttgaaggaaa aatcgc 36

<210> 4
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 4
tgcctcgagt tatcagacca tgtacatccc gc 32

<210> 5
<211> 248
<212> PRT
<213> Bacillus subtilis

<400> 5
Met Asp Met Leu Asn Asp Lys Thr Ala Ile Val Thr Gly Ala Ser Arg
1 5 10 15
Gly Ile Gly Arg Ser Ile Ala Leu Ala Leu Ala Lys Ser Gly Ala Asn
20 25 30
Val Val Val Asn Tyr Ser Gly Asn Glu Ala Lys Ala Asn Glu Val Val
35 40 45
Asp Glu Ile Lys Ser Met Gly Arg Lys Ala Ile Ala Val Lys Ala Asp
50 55 60
Val Ser Asn Pro Glu Asp Val Gln Asn Met Ile Lys Glu Thr Leu Ser
65 70 75 80
Val Phe Ser Thr Ile Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg
85 90 95
Asp Asn Leu Ile Met Arg Met Lys Glu Asp Glu Trp Asp Asp Val Ile
100 105 110
Asn Ile Asn Leu Lys Gly Val Phe Asn Cys Thr Lys Ala Val Thr Arg
115 120 125
Gln Met Met Lys Gln Arg Ser Gly Arg Ile Ile Asn Val Ser Ser Ile
130 135 140
Val Gly Val Ser Gly Asn Pro Gly Gln Ala Asn Tyr Val Ala Ala Lys

145		150		155		160
Ala Gly Val Ile Gly Leu Thr Lys Ser Ser Ala Lys Glu Leu Ala Ser						
	165			170		175
Arg Asn Ile Thr Val Asn Ala Ile Ala Pro Gly Phe Ile Ser Thr Asp						
	180			185		190
Met Thr Asp Lys Leu Ala Lys Asp Val Gln Asp Glu Met Leu Lys Gln						
	195			200		205
Ile Pro Leu Ala Arg Phe Gly Glu Pro Ser Asp Val Ser Ser Val Val						
	210			215		220
Thr Phe Leu Ala Ser Glu Gly Ala Arg Tyr Met Thr Gly Gln Thr Leu						
	225			230		235
						240
His Ile Asp Gly Gly Met Val Met						
	245					

<210> 6
 <211> 747
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(747)

<400> 6	
atg gat atg ctt aat gat aaa acg gct att gtc act ggc gca tcc cgc	48
Met Asp Met Leu Asn Asp Lys Thr Ala Ile Val Thr Gly Ala Ser Arg	
1 5 10 15	
gga atc ggc cgc tca atc gcc ctt gct ctg gca aaa agc gga gca aat	96
Gly Ile Gly Arg Ser Ile Ala Leu Ala Leu Ala Lys Ser Gly Ala Asn	
20 25 30	
gtt gtc gtg aac tac tcc ggc aat gaa gcg aaa gca aat gaa gtg gta	144
Val Val Val Asn Tyr Ser Gly Asn Glu Ala Lys Ala Asn Glu Val Val	
35 40 45	
gat gaa atc aaa tca atg ggc aga aaa gca att gct gta aaa gcg gat	192
Asp Glu Ile Lys Ser Met Gly Arg Lys Ala Ile Ala Val Lys Ala Asp	
50 55 60	
gta tca aat ccc gaa gat gta caa aac atg ata aaa gaa aca ttg tct	240
Val Ser Asn Pro Glu Asp Val Gln Asn Met Ile Lys Glu Thr Leu Ser	
65 70 75 80	
gtt ttt tct acg att gac att ctg gtt aat aat gcg gga att aca aga	288

Val	Phe	Ser	Thr	Ile	Asp	Ile	Leu	Val	Asn	Asn	Ala	Gly	Ile	Thr	Arg	
				85					90					95		
gac	aat	ctc	atc	atg	aga	atg	aaa	gaa	gac	gaa	tgg	gat	gac	gtc	att	336
Asp	Asn	Leu	Ile	Met	Arg	Met	Lys	Glu	Asp	Glu	Trp	Asp	Asp	Val	Ile	
			100					105					110			
aac	att	aac	ctg	aag	ggg	gtt	ttc	aac	tgc	aca	aaa	gct	gtt	aca	aga	384
Asn	Ile	Asn	Leu	Lys	Gly	Val	Phe	Asn	Cys	Thr	Lys	Ala	Val	Thr	Arg	
		115					120					125				
caa	atg	atg	aaa	cag	cgt	tca	ggc	cgc	att	att	aac	gta	tcg	tct	atc	432
Gln	Met	Met	Lys	Gln	Arg	Ser	Gly	Arg	Ile	Ile	Asn	Val	Ser	Ser	Ile	
	130					135					140					
gtc	ggc	gtc	agc	gga	aac	cct	gga	caa	gcc	aac	tac	gtg	gct	gca	aaa	480
Val	Gly	Val	Ser	Gly	Asn	Pro	Gly	Gln	Ala	Asn	Tyr	Val	Ala	Ala	Lys	
	145				150					155					160	
gcc	ggc	gtc	atc	ggg	tta	acc	aaa	tct	tct	gct	aaa	gag	ctc	gcc	agc	528
Ala	Gly	Val	Ile	Gly	Leu	Thr	Lys	Ser	Ser	Ala	Lys	Glu	Leu	Ala	Ser	
				165				170						175		
cga	aat	att	acg	gta	aac	gca	ata	gcg	cca	gga	ttt	atc	tca	act	gat	576
Arg	Asn	Ile	Thr	Val	Asn	Ala	Ile	Ala	Pro	Gly	Phe	Ile	Ser	Thr	Asp	
			180					185					190			
atg	aca	gat	aaa	ctt	gca	aaa	gac	gtt	caa	gac	gaa	atg	ctg	aaa	caa	624
Met	Thr	Asp	Lys	Leu	Ala	Lys	Asp	Val	Gln	Asp	Glu	Met	Leu	Lys	Gln	
		195					200					205				
att	ccg	ctc	gcg	cgc	ttt	ggg	gaa	cct	agc	gat	gtc	agc	agt	gtt	gtc	672
Ile	Pro	Leu	Ala	Arg	Phe	Gly	Glu	Pro	Ser	Asp	Val	Ser	Ser	Val	Val	
	210					215					220					
acg	ttc	cta	gct	tca	gag	gga	gct	cgt	tat	atg	aca	ggc	caa	acg	ctt	720
Thr	Phe	Leu	Ala	Ser	Glu	Gly	Ala	Arg	Tyr	Met	Thr	Gly	Gln	Thr	Leu	
	225				230					235					240	
cat	att	gac	ggc	gga	atg	gtg	atg	taa								747
His	Ile	Asp	Gly	Gly	Met	Val	Met									
				245												

<210> 7

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially

Synthesized Primer Sequence

<400> 7
ggaccatgga tatgcttaat gataaaacgg cta 33

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 8
gagaagcttc tcgagttaca tcaccattcc gccg 34

<210> 9
<211> 246
<212> PRT
<213> Ralstonia eutropha

<400> 9
Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
1 5 10 15
Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
20 25 30
Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
35 40 45
Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
50 55 60
Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
65 70 75 80
Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
85 90 95
Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
100 105 110
Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
115 120 125
Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
130 135 140

Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
145 150 155 160

His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
165 170 175

Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
180 185 190

Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
195 200 205

Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
210 215 220

Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
225 230 235 240

Gly Gly Leu His Met Gly
245

<210> 10
<211> 741
<212> DNA
<213> Ralstonia eutropha

<220>
<221> CDS
<222> (1)..(738)

<400> 10
atg act cag cgc att gcg tat gtg acc ggc ggc atg ggt ggt atc gga 48
Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
1 5 10 15

acc gcc att tgc cag cgg ctg gcc aag gat ggc ttt cgt gtg gtg gcc 96
Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
20 25 30

ggt tgc ggc ccc aac tcg ccg cgc cgc gaa aag tgg ctg gag cag cag 144
Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
35 40 45

aag gcc ctg ggc ttc gat ttc att gcc tcg gaa ggc aat gtg gct gac 192
Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
50 55 60

tgg gac tcg acc aag acc gca ttc gac aag gtc aag tcc gag gtc ggc 240
Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
65 70 75 80

gag gtt gat gtg ctg atc aac aac gcc ggt atc acc cgc gac gtg gtg	288
Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val	
85 90 95	
ttc cgc aag atg acc cgc gcc gac tgg gat gcg gtg atc gac acc aac	336
Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn	
100 105 110	
ctg acc tcg ctg ttc aac gtc acc aag cag gtg atc gac ggc atg gcc	384
Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala	
115 120 125	
gac cgt ggc tgg ggc cgc atc gtc aac atc tcg tcg gtg aac ggg cag	432
Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln	
130 135 140	
aag ggc cag ttc ggc cag acc aac tac tcc acc gcc aag gcc ggc ctg	480
Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu	
145 150 155 160	
cat ggc ttc acc atg gca ctg gcg cag gaa gtg gcg acc aag ggc gtg	528
His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val	
165 170 175	
acc gtc aac acg gtc tct ccg ggc tat atc gcc acc gac atg gtc aag	576
Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys	
180 185 190	
gcg atc cgc cag gac gtg ctc gac aag atc gtc gcg acg atc ccg gtc	624
Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val	
195 200 205	
aag cgc ctg ggc ctg ccg gaa gag atc gcc tcg atc tgc gcc tgg ttg	672
Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu	
210 215 220	
tcg tcg gag gag tcc ggt ttc tcg acc ggc gcc gac ttc tcg ctc aac	720
Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn	
225 230 235 240	
ggc ggc ctg cat atg ggc taa	741
Gly Gly Leu His Met Gly	
245	

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially

Synthesized Primer Sequence

<400> 11
agtggatcca atgactcagc gcattgcgta 30

<210> 12
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 12
aacaagcttc tcgagtttag ccatatgcag gccgc 35

<210> 13
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Sequence

<400> 13
aattctcgag taatctagag gaattctaaa a 31

<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Sequence

<400> 14
ctagtttttag aattcctcta gattactcga g 31

<210> 15
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 15
gaggaattca tacatgtatc cagatttaaa aggaa 35

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificially
Synthesized Primer Sequence

<400> 16
ggtaagcttt cattaaccgc ggcctgcctg 30

<210> 17
<211> 806
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (12)..(794)

<400> 17
ggaattcata c atg tat cca gat tta aaa gga aaa gtc gtc gct att aca 50
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr
1 5 10
gga gct gct tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag 98
Gly Ala Ala Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys
15 20 25
gag cag gca aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg 146
Glu Gln Ala Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro
30 35 40 45
aac gag gta aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc 194
Asn Glu Val Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val
50 55 60
gtc caa gga gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa 242
Val Gln Gly Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln
65 70 75
acg gca att aag gag ttc ggc aca ctc gat att atg att aat aat gcc 290
Thr Ala Ile Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala
80 85 90

ggt ctt gaa aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg	338
Gly Leu Glu Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp	
95 100 105	
gat aaa gtc atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt	386
Asp Lys Val Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg	
110 115 120 125	
gaa gcg att aaa tat ttc gta gaa aac gat atc aag gga aat gtc att	434
Glu Ala Ile Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile	
130 135 140	
aac atg tcc agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac	482
Asn Met Ser Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His	
145 150 155	
tat gcg gca agt aaa ggc ggg ata aag ctg atg aca gaa aca tta gcg	530
Tyr Ala Ala Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala	
160 165 170	
ttg gaa tac gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt	578
Leu Glu Tyr Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly	
175 180 185	
gcg atc aac acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag	626
Ala Ile Asn Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln	
190 195 200 205	
aaa gct gat gta gaa agc atg att cca atg gga tat atc ggc gaa ccg	674
Lys Ala Asp Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro	
210 215 220	
gag gag atc gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc	722
Glu Glu Ile Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser	
225 230 235	
tac gtc aca ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat	770
Tyr Val Thr Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr	
240 245 250	
cct tca ttc cag gca ggc cgc ggt taatgaaagc tt	806
Pro Ser Phe Gln Ala Gly Arg Gly	
255 260	

<210> 18

<211> 261

<212> PRT

<213> Bacillus subtilis

<400> 18

Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
1 5 10 15

Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
20 25 30

Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
35 40 45

Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
50 55 60

Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
65 70 75 80

Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
85 90 95

Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
100 105 110

Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
115 120 125

Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
130 135 140

Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
145 150 155 160

Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
165 170 175

Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
180 185 190

Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
195 200 205

Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
210 215 220

Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
225 230 235 240

Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
245 250 255

Gln Ala Gly Arg Gly
260

CCRC" 005000

What is claimed is:

1. A method for producing (S)-4-halo-3-hydroxybutyric acid ester comprising asymmetrically reducing 4-halo-acetoacetic acid ester or its derivatives with β -ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase.

2. The method of claim 1, wherein said β -ketoacyl carrier protein reductase is derived from *Escherihia coli*.

3. The method of claim 1, wherein said β -ketoacyl carrier protein reductase is selected from the group consisting of:

- (a) a protein comprising the amino acid sequence of SEQ ID NO: 1;
- (b) a protein comprising a modified amino acid sequence of SEQ ID NO: 1 in which one or more amino acid residues are added, deleted, or substituted and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester; and
- (c) a protein encoded by DNA hybridizable with the DNA comprising the nucleotide sequence of SEQ ID NO: 2 and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester.

4. The method of claim 1, wherein said β -ketoacyl-acyl carrier protein reductase is derived from microorganisms belonging to the genus *Bacillus*.

5. The method of claim 4, wherein said β -ketoacyl-acyl carrier protein reductase is derived from *Bacillus subtilis*.

6. The method of claim 1, wherein said β -ketoacyl-acyl carrier protein reductase is selected from the group consisting of:

- (a) a protein comprising the amino acid sequence of SEQ ID NO: 5;
- (b) a protein comprising a modified amino acid sequence of SEQ ID NO: 5 in which one or more amino acid residues are added, deleted,

or substituted and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester; and

(c) a protein encoded by DNA hybridizable with the DNA comprising the nucleotide sequence of SEQ ID NO: 6 and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester.

7. A method for producing (S)-4-halo-3-hydroxybutyric acid ester comprising asymmetrically reducing 4-halo-acetoacetic acid ester or its derivatives with acetoacetyl-CoA reductase constituting the poly- β -hydroxy fatty acid biosynthesis system.

8. A method of claim 7, wherein said acetoacetyl-CoA reductase is derived from microorganisms belonging to the genus *Ralstonia*.

9. The method of claim 8, wherein said acetoacetyl-CoA reductase is derived from *Ralstonia eutropha*.

10. The method of claim 7, wherein said acetoacetyl-CoA reductase is selected from the group consisting of:

(a) a protein comprising the amino acid sequence of SEQ ID NO: 9;

(b) a protein comprising a modified amino acid sequence of SEQ ID NO: 9 in which one or more amino acid residues are added, deleted, or substituted and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester; and

(c) a protein encoded by DNA hybridizable with the DNA comprising the nucleotide sequence of SEQ ID NO: 10 and capable of asymmetrically reducing 4-haloacetoacetic acid ester or its derivatives to produce (S)-4-halo-3-hydroxybutyric acid ester.

11. The method of claim 1, wherein said 4-haloacetoacetic

acid ester is 4-chloroacetoacetic acid ester.

12. The method of claim 7, wherein said 4-haloacetoacetic acid ester is 4-chloroacetoacetic acid ester.

13. The method of claim 1, wherein said 4-haloacetoacetic acid ester is ethyl 4-chloroacetoacetate.

14. The method of claim 7, wherein said 4-haloacetoacetic acid ester is ethyl 4-chloroacetoacetate.

15. The method of claim 1, wherein said method uses a microorganism capable of producing β -ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase and an enzyme catalyzing production of NAD(P)H from NAD(P)⁺.

16. The method of claim 15, wherein said microorganism is a recombinant microorganism into which heterologous or homologous DNA encoding the β -ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase and heterologous or homologous DNA encoding an enzyme catalyzing production of NAD(P)H from NAD(P)⁺, and is capable of expressing both enzymes.

17. The method of claim 16, wherein said microorganism is *Escherihia coli*.

18. The method of any one of claims 15, wherein said enzyme catalyzing production of NAD(P)H from NAD(P)⁺ is glucose dehydrogenase.

19. The method of claim 7, wherein said method uses a microorganism capable of producing acetoacetyl-CoA reductase constituting the poly- β -hydroxy fatty acid biosynthesis system and an enzyme catalyzing production of NAD(P)H from NAD(P)⁺.

20. The method of claim 19, wherein said microorganism is a recombinant microorganism into which heterologous or homologous DNA encoding acetoacetyl-CoA reductase constituting the poly- β -

21. The method of claim 20, wherein said microorganism is *Escherichia coli*.

22. The method of any one of claims 19, wherein said enzyme catalyzing production of NAD(P)H from NAD(P)⁺ is glucose dehydrogenase.

ABSTRACT OF THE DISCLOSURE

The present invention provides a method for preparing (S)-4-halo-3-hydroxybutyric acid ester comprises asymmetric reduction of 4-halo-acetoacetic acid ester using β -ketoacyl-acylcarrier protein reductase constituting Type II fatty acid synthase or acetoacetyl-CoA reductase constituting the poly- β -hydroxy fatty acid synthesis system. β -ketoacyl-acyl carrier protein reductase constituting Type II fatty acid synthase or acetoacetyl-CoA reductase constituting the poly- β -hydroxy fatty acid synthesis system has a extremely high reducing activity as well as stereoselectivity for (S)-4-chloro-3-hydroxybutyric acid ester. In addition, the enzyme exhibits almost no oxidizing activity toward either configuration of ethyl 4-chloro-3-hydroxybutyrate, performing only the reducing reaction of ethyl 4-chloroacetoacetate. Therefore, this enzyme can be used to efficiently produce (S)-4-halo-3-hydroxybutyric acid ester.

Fig. 1

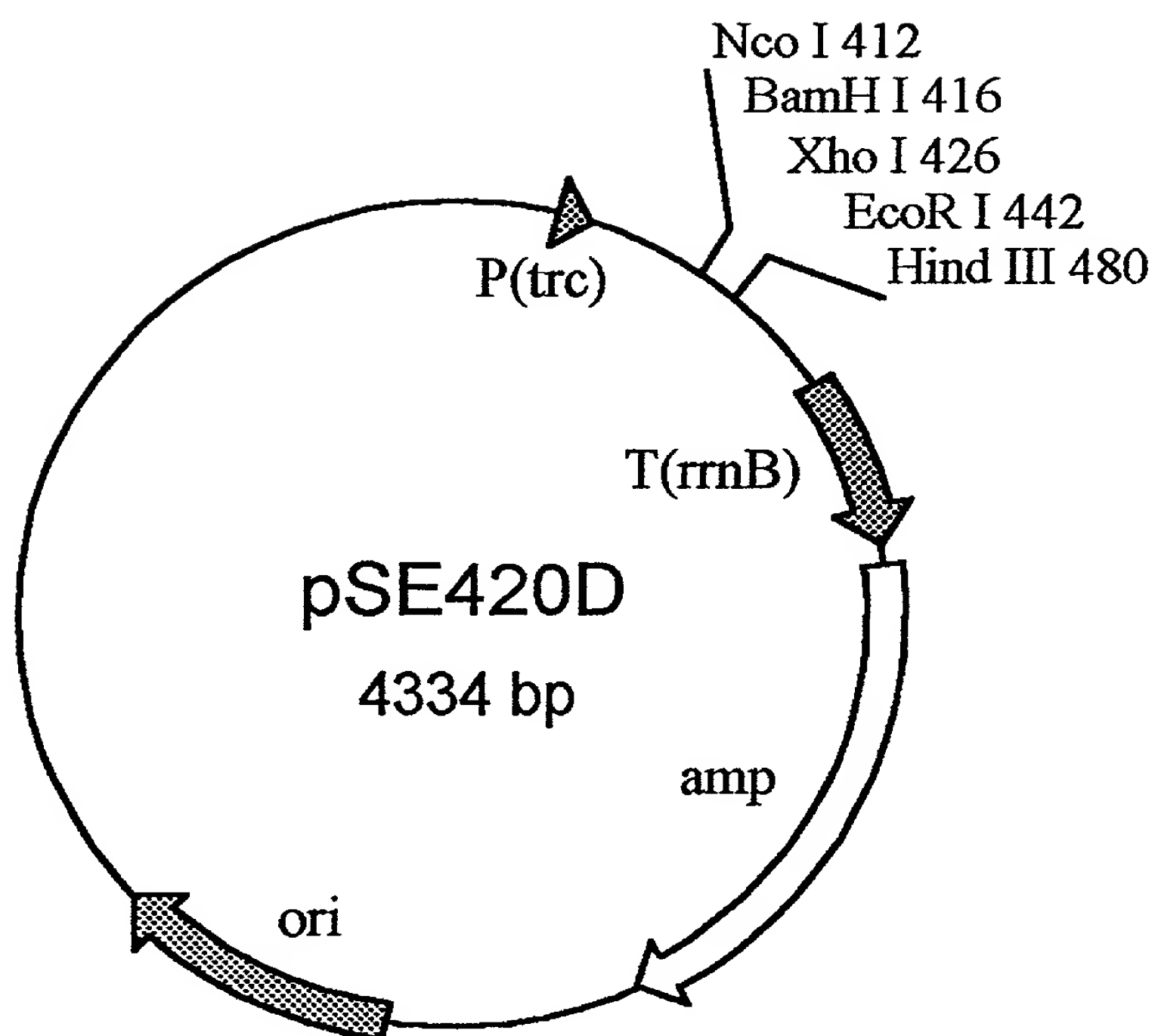


Fig. 2

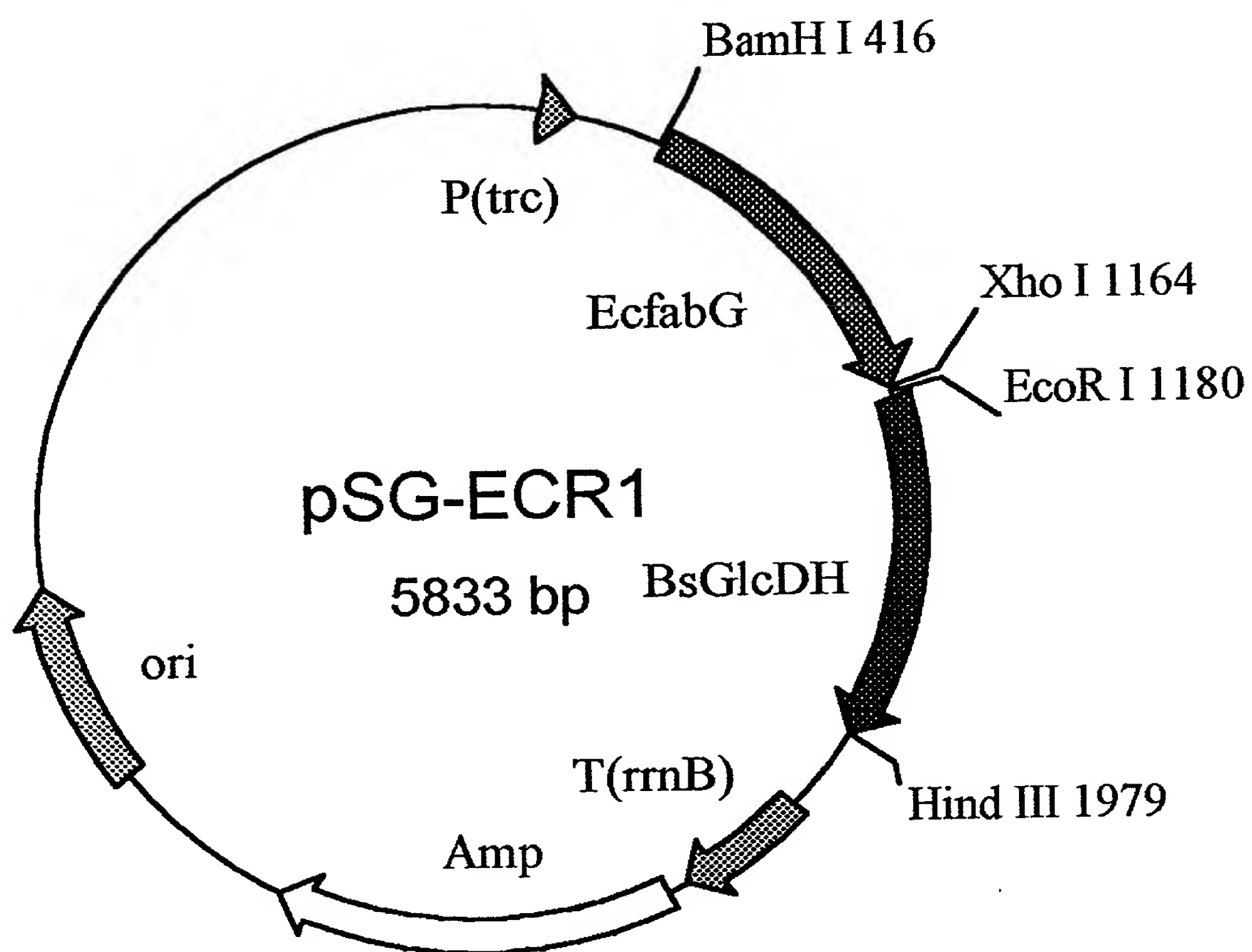


Fig. 3

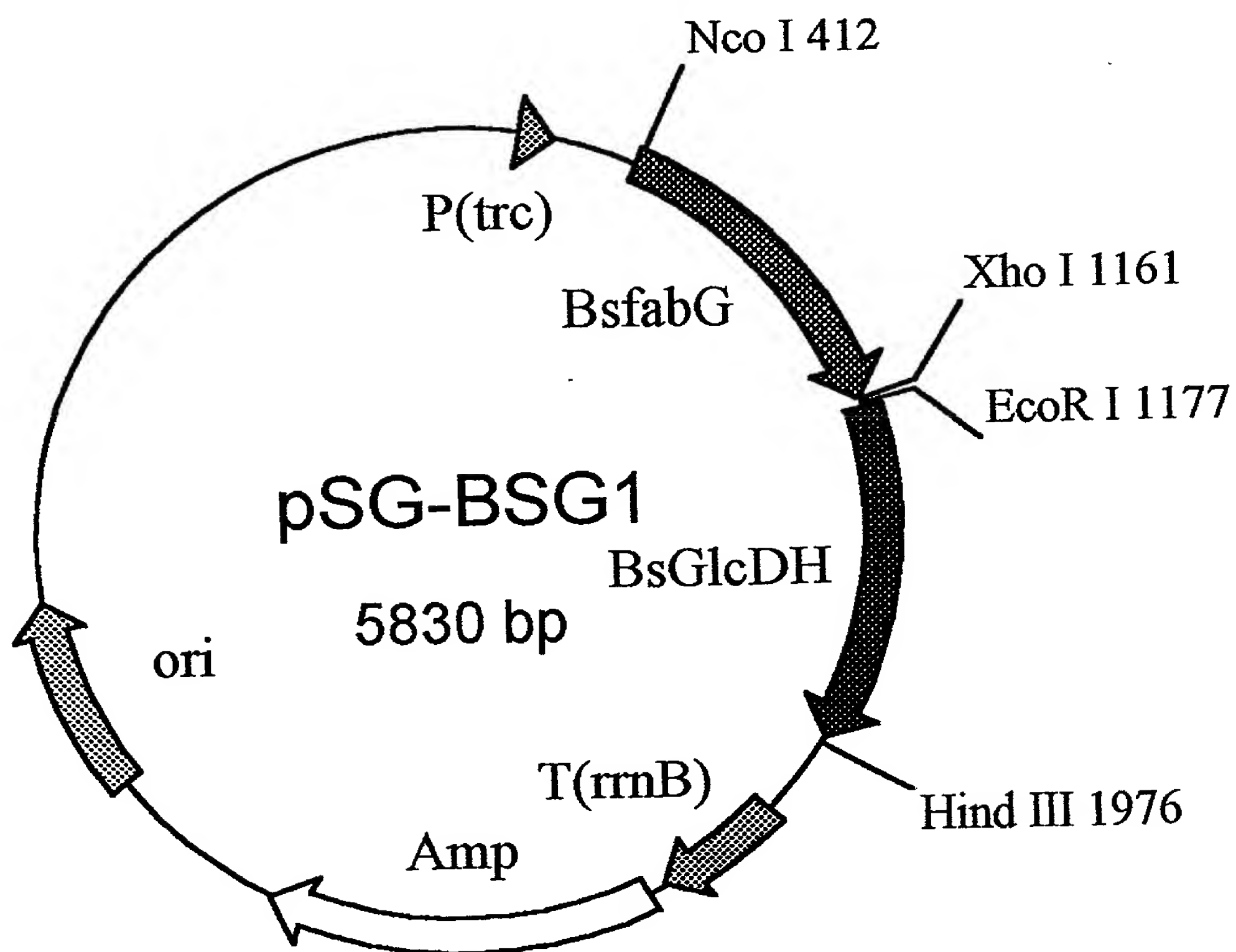
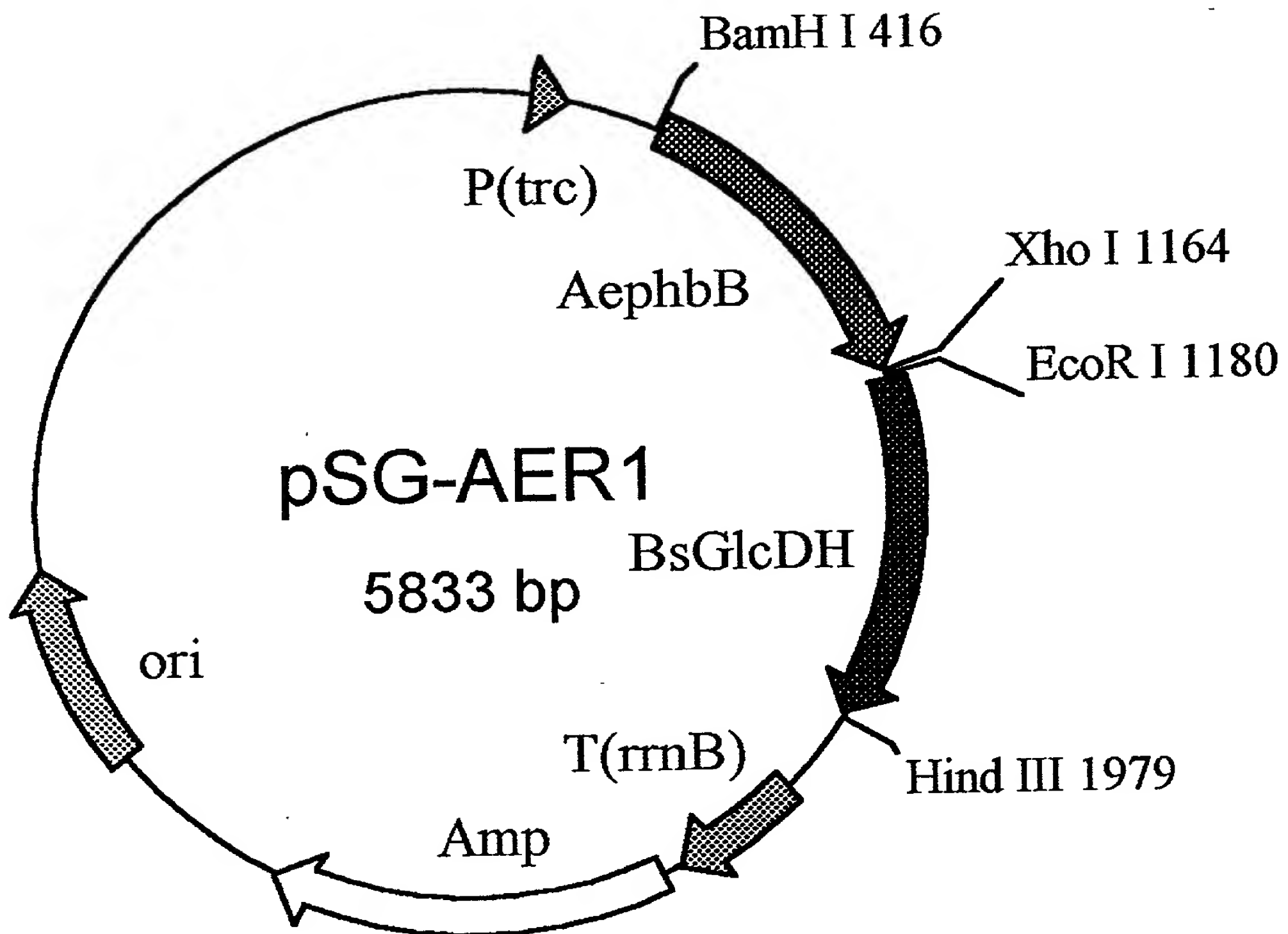


Fig. 4



COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled METHOD FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTYRIC ACID ESTER, the specification of which

☒ is attached hereto.

☐ was filed on _____ as Application Serial No. _____
and was amended on _____.

☐ was described and claimed in PCT International Application No. _____
filed on _____ and as amended under PCT Article 19 on _____.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information I know to be material to patentability in accordance with Title 37, Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate or of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign application for patent or inventor's certificate or any PCT international application(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed:

COUNTRY	APPLICATION NO.	FILING DATE	PRIORITY CLAIMED
<u>Japan</u>	<u>10-126507</u>	<u>May 8, 1998</u>	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No
<u>Japan</u>	<u>10-300178</u>	<u>October 21, 1998</u>	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No
<u>Japan</u>	<u>11-98205</u>	<u>April 5, 1999</u>	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No

I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

Janis K. Fraser, Reg. No. 34,819; J. Peter Fasse, Reg. No. 32,983; John W. Freeman, Reg. No. 29,066; Timothy A. French, Reg. No. 30,175; Eldora L. Ellison, Reg. No. 39,967; Anita L. Meiklejohn, Reg. No. 35,283; and Ralph A. Mittelberger, Reg. No. 33,195.

Address all telephone calls to Janis K. Fraser at telephone number 617/542-5070.

Address all correspondence to Janis K. Fraser, Fish & Richardson P.C., 225 Franklin Street, Boston, MA 02110-2804.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

COMBINED DECLARATION AND POWER OF ATTORNEY CONTINUED

Full Name of Inventor: Hiroaki Yamamoto

Inventor's Signature: _____ Date: _____

Residence Address: Ibaraki, Japan

Citizen of: Japan

Post Office Address: 1-14-14-103, Sengen, Tsukuba-Shi, Ibaraki 305-0047 Japan

371273.B11

SEQUENCE LISTING

<110> Yamamoto, Hiroaki

<120> METHOD FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTYRIC ACID ESTER

<130> 06501/030001

<150> JP 1998-126507

<151> 1998-10-21

<150> JP 1998-300178

<151> 1998-10-21

<160> 18

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 244

<212> PRT

<213> Escherichia coli

<400> 1

Met	Asn	Phe	Glu	Gly	Lys	Ile	Ala	Leu	Val	Thr	Gly	Ala	Ser	Arg	Gly
1				5					10					15	
Ile	Gly	Arg	Ala	Ile	Ala	Glu	Thr	Leu	Ala	Ala	Arg	Gly	Ala	Lys	Val
			20					25					30		
Ile	Gly	Thr	Ala	Thr	Ser	Glu	Asn	Gly	Ala	Gln	Ala	Ile	Ser	Asp	Tyr
		35				40						45			
Leu	Gly	Ala	Asn	Gly	Lys	Gly	Leu	Met	Leu	Asn	Val	Thr	Asp	Pro	Ala
	50					55				60					
Ser	Ile	Glu	Ser	Val	Leu	Glu	Lys	Ile	Arg	Ala	Glu	Phe	Gly	Glu	Val
	65				70				75					80	
Asp	Ile	Leu	Val	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Asn	Leu	Leu	Met
				85					90					95	
Arg	Met	Lys	Asp	Glu	Glu	Trp	Asn	Asp	Ile	Ile	Glu	Thr	Asn	Leu	Ser
			100					105					110		
Ser	Val	Phe	Arg	Leu	Ser	Lys	Ala	Val	Met	Arg	Ala	Met	Met	Lys	Lys
		115					120					125			
Arg	His	Gly	Arg	Ile	Ile	Thr	Ile	Gly	Ser	Val	Val	Gly	Thr	Met	Gly
	130					135						140			
Asn	Gly	Gly	Gln	Ala	Asn	Tyr	Ala	Ala	Ala	Lys	Ala	Gly	Leu	Ile	Gly
	145				150					155				160	
Phe	Ser	Lys	Ser	Leu	Ala	Arg	Glu	Val	Ala	Ser	Arg	Gly	Ile	Thr	Val
			165					170					175		
Asn	Val	Val	Ala	Pro	Gly	Phe	Ile	Glu	Thr	Asp	Met	Thr	Arg	Ala	Leu
			180					185					190		
Ser	Asp	Asp	Gln	Arg	Ala	Gly	Ile	Leu	Ala	Gln	Val	Pro	Ala	Gly	Arg
	195					200						205			
Leu	Gly	Gly	Ala	Gln	Glu	Ile	Ala	Asn	Ala	Val	Ala	Phe	Leu	Ala	Ser
	210					215					220				
Asp	Glu	Ala	Ala	Tyr	Ile	Thr	Gly	Glu	Thr	Leu	His	Val	Asn	Gly	Gly
	225				230					235				240	
Met	Tyr	Met	Val												

<210> 2

<211> 735

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(732)

<400> 2

atg	aat	ttt	gaa	gga	aaa	atc	gca	ctg	gta	acc	ggt	gca	agc	cgc	gga	48
Met	Asn	Phe	Glu	Gly	Lys	Ile	Ala	Leu	Val	Thr	Gly	Ala	Ser	Arg	Gly	
1				5					10					15		
att	ggc	cgc	gca	att	gct	gaa	acg	ctc	gca	gcc	cgt	ggc	gcg	aaa	gtt	96
Ile	Gly	Arg	Ala	Ile	Ala	Glu	Thr	Leu	Ala	Ala	Arg	Gly	Ala	Lys	Val	
			20					25					30			
att	ggc	act	gcg	acc	agt	gaa	aat	ggc	gct	cag	gcg	atc	agt	gat	tat	144
Ile	Gly	Thr	Ala	Thr	Ser	Glu	Asn	Gly	Ala	Gln	Ala	Ile	Ser	Asp	Tyr	
		35					40					45				
tta	ggt	gcc	aac	ggc	aaa	ggt	ctg	atg	ttg	aat	gtg	acc	gac	ccg	gca	192
Leu	Gly	Ala	Asn	Gly	Lys	Gly	Leu	Met	Leu	Asn	Val	Thr	Asp	Pro	Ala	
	50					55					60					
tct	atc	gaa	tct	gtt	ctg	gaa	aaa	att	cgc	gca	gaa	ttt	ggt	gaa	gtg	240
Ser	Ile	Glu	Ser	Val	Leu	Glu	Lys	Ile	Arg	Ala	Glu	Phe	Gly	Glu	Val	
	65				70					75					80	
gat	atc	ctg	gtc	aat	aat	gcc	ggt	atc	act	cgt	gat	aac	ctg	tta	atg	288
Asp	Ile	Leu	Val	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Asn	Leu	Leu	Met	
				85					90					95		
cga	atg	aaa	gat	gaa	gag	tgg	aac	gat	att	atc	gaa	acc	aac	ctt	tca	336
Arg	Met	Lys	Asp	Glu	Glu	Trp	Asn	Asp	Ile	Ile	Glu	Thr	Asn	Leu	Ser	
			100					105					110			
tct	gtt	ttc	cgt	ctg	tca	aaa	gcg	gta	atg	cgc	gct	atg	atg	aaa	aag	384
Ser	Val	Phe	Arg	Leu	Ser	Lys	Ala	Val	Met	Arg	Ala	Met	Met	Lys	Lys	
		115					120					125				
cgt	cat	ggt	cgt	att	atc	act	atc	ggt	tct	gtg	gtt	ggt	acc	atg	gga	432
Arg	His	Gly	Arg	Ile	Ile	Thr	Ile	Gly	Ser	Val	Val	Gly	Thr	Met	Gly	
	130					135					140					
aat	ggc	ggt	cag	gcc	aac	tac	gct	gcg	gcg	aaa	gcg	ggc	ttg	atc	ggc	480
Asn	Gly	Gly	Gln	Ala	Asn	Tyr	Ala	Ala	Ala	Lys	Ala	Gly	Leu	Ile	Gly	
	145				150					155					160	
ttc	agt	aaa	tca	ctg	gcg	cgc	gaa	gtt	gcg	tca	cgc	ggt	att	act	gta	528
Phe	Ser	Lys	Ser	Leu	Ala	Arg	Glu	Val	Ala	Ser	Arg	Gly	Ile	Thr	Val	
				165					170					175		
aac	gtt	gtt	gct	ccg	ggc	ttt	att	gaa	acg	gac	atg	aca	cgt	gcg	ctg	576
Asn	Val	Val	Ala	Pro	Gly	Phe	Ile	Glu	Thr	Asp	Met	Thr	Arg	Ala	Leu	
			180					185					190			
agc	gat	gac	cag	cgt	gcg	ggt	atc	ctg	gcg	cag	gtt	cct	gcg	ggt	cgc	624
Ser	Asp	Asp	Gln	Arg	Ala	Gly	Ile	Leu	Ala	Gln	Val	Pro	Ala	Gly	Arg	
		195					200					205				
ctc	ggc	ggc	gca	cag	gaa	atc	gcc	aac	gcg	gtt	gca	ttc	ctg	gca	tcc	672
Leu	Gly	Gly	Ala	Gln	Glu	Ile	Ala	Asn	Ala	Val	Ala	Phe	Leu	Ala	Ser	
	210					215					220					

Met	Thr	Asp	Lys	Leu	Ala	Lys	Asp	Val	Gln	Asp	Glu	Met	Leu	Lys	Gln
		195					200					205			
Ile	Pro	Leu	Ala	Arg	Phe	Gly	Glu	Pro	Ser	Asp	Val	Ser	Ser	Val	Val
	210					215					220				
Thr	Phe	Leu	Ala	Ser	Glu	Gly	Ala	Arg	Tyr	Met	Thr	Gly	Gln	Thr	Leu
225					230					235					240
His	Ile	Asp	Gly	Gly	Met	Val	Met								
				245											

<210> 6
 <211> 747
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)...(744)

<400> 6

atg	gat	atg	ctt	aat	gat	aaa	acg	gct	att	gtc	act	ggc	gca	tcc	cgc	48
Met	Asp	Met	Leu	Asn	Asp	Lys	Thr	Ala	Ile	Val	Thr	Gly	Ala	Ser	Arg	
1				5					10					15		
gga	atc	ggc	cgc	tca	atc	gcc	ctt	gct	ctg	gca	aaa	agc	gga	gca	aat	96
Gly	Ile	Gly	Arg	Ser	Ile	Ala	Leu	Ala	Leu	Ala	Lys	Ser	Gly	Ala	Asn	
			20					25					30			
gtt	gtc	gtg	aac	tac	tcc	ggc	aat	gaa	gcg	aaa	gca	aat	gaa	gtg	gta	144
Val	Val	Val	Asn	Tyr	Ser	Gly	Asn	Glu	Ala	Lys	Ala	Asn	Glu	Val	Val	
			35				40					45				
gat	gaa	atc	aaa	tca	atg	ggc	aga	aaa	gca	att	gct	gta	aaa	gcg	gat	192
Asp	Glu	Ile	Lys	Ser	Met	Gly	Arg	Lys	Ala	Ile	Ala	Val	Lys	Ala	Asp	
	50					55					60					
gta	tca	aat	ccc	gaa	gat	gta	caa	aac	atg	ata	aaa	gaa	aca	ttg	tct	240
Val	Ser	Asn	Pro	Glu	Asp	Val	Gln	Asn	Met	Ile	Lys	Glu	Thr	Leu	Ser	
65					70				75					80		
gtt	ttt	tct	acg	att	gac	att	ctg	gtt	aat	aat	gcg	gga	att	aca	aga	288
Val	Phe	Ser	Thr	Ile	Asp	Ile	Leu	Val	Asn	Asn	Ala	Gly	Ile	Thr	Arg	
				85					90					95		
gac	aat	ctc	atc	atg	aga	atg	aaa	gaa	gac	gaa	tgg	gat	gac	gtc	att	336
Asp	Asn	Leu	Ile	Met	Arg	Met	Lys	Glu	Asp	Glu	Trp	Asp	Asp	Val	Ile	
			100					105					110			
aac	att	aac	ctg	aag	ggc	gtt	ttc	aac	tgc	aca	aaa	gct	gtt	aca	aga	384
Asn	Ile	Asn	Leu	Lys	Gly	Val	Phe	Asn	Cys	Thr	Lys	Ala	Val	Thr	Arg	
			115				120					125				
caa	atg	atg	aaa	cag	cgt	tca	ggc	cgc	att	att	aac	gta	tcg	tct	atc	432
Gln	Met	Met	Lys	Gln	Arg	Ser	Gly	Arg	Ile	Ile	Asn	Val	Ser	Ser	Ile	
	130					135					140					
gtc	ggc	gtc	agc	gga	aac	cct	gga	caa	gcc	aac	tac	gtg	gct	gca	aaa	480
Val	Gly	Val	Ser	Gly	Asn	Pro	Gly	Gln	Ala	Asn	Tyr	Val	Ala	Ala	Lys	
145					150					155					160	
gcc	ggc	gtc	atc	ggt	tta	acc	aaa	tct	tct	gct	aaa	gag	ctc	gcc	agc	528
Ala	Gly	Val	Ile	Gly	Leu	Thr	Lys	Ser	Ser	Ala	Lys	Glu	Leu	Ala	Ser	
				165					170					175		

cga aat att acg gta aac gca ata gcg cca gga ttt atc tca act gat	576
Arg Asn Ile Thr Val Asn Ala Ile Ala Pro Gly Phe Ile Ser Thr Asp	
180 185 190	
atg aca gat aaa ctt gca aaa gac gtt caa gac gaa atg ctg aaa caa	624
Met Thr Asp Lys Leu Ala Lys Asp Val Gln Asp Glu Met Leu Lys Gln	
195 200 205	
att ccg ctc gcg cgc ttt ggt gaa cct agc gat gtc agc agt gtt gtc	672
Ile Pro Leu Ala Arg Phe Gly Glu Pro Ser Asp Val Ser Ser Val Val	
210 215 220	
acg ttc cta gct tca gag gga gct cgt tat atg aca ggc caa acg ctt	720
Thr Phe Leu Ala Ser Glu Gly Ala Arg Tyr Met Thr Gly Gln Thr Leu	
225 230 235 240	
cat att gac ggc gga atg gtg atg taa	747
His Ile Asp Gly Gly Met Val Met	
245	

<210> 7
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 7
 ggaccatgga tatgcttaat gataaaacgg cta 33

<210> 8
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 8
 gagaagcttc tcgagttaca tcaccattcc gccg 34

<210> 9
 <211> 246
 <212> PRT
 <213> Ralstonia eutropha

<400> 9
 Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
 1 5 10 15
 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
 20 25 30
 Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
 35 40 45
 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
 50 55 60
 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
 65 70 75 80

Glu	Val	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Val	Val	
				85					90					95		
Phe	Arg	Lys	Met	Thr	Arg	Ala	Asp	Trp	Asp	Ala	Val	Ile	Asp	Thr	Asn	
			100					105					110			
Leu	Thr	Ser	Leu	Phe	Asn	Val	Thr	Lys	Gln	Val	Ile	Asp	Gly	Met	Ala	
		115					120					125				
Asp	Arg	Gly	Trp	Gly	Arg	Ile	Val	Asn	Ile	Ser	Ser	Val	Asn	Gly	Gln	
	130					135					140					
Lys	Gly	Gln	Phe	Gly	Gln	Thr	Asn	Tyr	Ser	Thr	Ala	Lys	Ala	Gly	Leu	
145					150					155					160	
His	Gly	Phe	Thr	Met	Ala	Leu	Ala	Gln	Glu	Val	Ala	Thr	Lys	Gly	Val	
				165					170					175		
Thr	Val	Asn	Thr	Val	Ser	Pro	Gly	Tyr	Ile	Ala	Thr	Asp	Met	Val	Lys	
			180					185					190			
Ala	Ile	Arg	Gln	Asp	Val	Leu	Asp	Lys	Ile	Val	Ala	Thr	Ile	Pro	Val	
		195					200					205				
Lys	Arg	Leu	Gly	Leu	Pro	Glu	Glu	Ile	Ala	Ser	Ile	Cys	Ala	Trp	Leu	
	210					215					220					
Ser	Ser	Glu	Glu	Ser	Gly	Phe	Ser	Thr	Gly	Ala	Asp	Phe	Ser	Leu	Asn	
225					230					235					240	
Gly	Gly	Leu	His	Met	Gly											
				245												

<210> 10
 <211> 741
 <212> DNA
 <213> Ralstonia eutropha

<220>
 <221> CDS
 <222> (1)...(738)

<400> 10																
atg	act	cag	cgc	att	gcg	tat	gtg	acc	ggc	ggc	atg	ggg	ggg	atc	gga	48
Met	Thr	Gln	Arg	Ile	Ala	Tyr	Val	Thr	Gly	Gly	Met	Gly	Gly	Ile	Gly	
1				5					10					15		
acc gcc att tgc cag cgg ctg gcc aag gat ggc ttt cgt gtg gtg gcc																96
Thr	Ala	Ile	Cys	Gln	Arg	Leu	Ala	Lys	Asp	Gly	Phe	Arg	Val	Val	Ala	
			20					25					30			
ggg tgc ggc ccc aac tcg ccg cgc cgc gaa aag tgg ctg gag cag cag																144
Gly	Cys	Gly	Pro	Asn	Ser	Pro	Arg	Arg	Glu	Lys	Trp	Leu	Glu	Gln	Gln	
		35					40					45				
aag gcc ctg ggc ttc gat ttc att gcc tcg gaa ggc aat gtg gct gac																192
Lys	Ala	Leu	Gly	Phe	Asp	Phe	Ile	Ala	Ser	Glu	Gly	Asn	Val	Ala	Asp	
	50					55				60						
tgg gac tcg acc aag acc gca ttc gac aag gtc aag tcc gag gtc ggc																240
Trp	Asp	Ser	Thr	Lys	Thr	Ala	Phe	Asp	Lys	Val	Lys	Ser	Glu	Val	Gly	
65					70				75						80	
gag gtt gat gtg ctg atc aac aac gcc ggt atc acc cgc gac gtg gtg																288
Glu	Val	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Val	Val	
				85					90					95		
ttc cgc aag atg acc cgc gcc gac tgg gat gcg gtg atc gac acc aac																336
Phe	Arg	Lys	Met	Thr	Arg	Ala	Asp	Trp	Asp	Ala	Val	Ile	Asp	Thr	Asn	
			100					105					110			

ctg acc tcg ctg ttc aac gtc acc aag cag gtg atc gac ggc atg gcc	384
Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala	
115 120 125	
gac cgt ggc tgg ggc cgc atc gtc aac atc tcg tcg gtg aac ggg cag	432
Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln	
130 135 140	
aag ggc cag ttc ggc cag acc aac tac tcc acc gcc aag gcc ggc ctg	480
Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu	
145 150 155 160	
cat ggc ttc acc atg gca ctg gcg cag gaa gtg gcg acc aag ggc gtg	528
His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val	
165 170 175	
acc gtc aac acg gtc tct ccg ggc tat atc gcc acc gac atg gtc aag	576
Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys	
180 185 190	
gcg atc cgc cag gac gtg ctc gac aag atc gtc gcg acg atc ccg gtc	624
Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val	
195 200 205	
aag cgc ctg ggc ctg ccg gaa gag atc gcc tcg atc tgc gcc tgg ttg	672
Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu	
210 215 220	
tcg tcg gag gag tcc ggt ttc tcg acc ggc gcc gac ttc tcg ctc aac	720
Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn	
225 230 235 240	
ggc ggc ctg cat atg ggc taa	741
Gly Gly Leu His Met Gly	
245	

<210> 11
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 11	30
agtggatcca atgactcagc gcattgcgta	

<210> 12
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 12	35
aacaagcttc tcgagttagc ccatatgcag gccgc	

<210> 13
 <211> 31
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Artificially synthesized sequence
 <400> 13
 aattctcgag taatctagag gaattctaaa a 31
 <210> 14
 <211> 31
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Artificially synthesized sequence
 <400> 14
 ctagtttttag aattcctcta gattactcga g 31
 <210> 15
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Artificially synthesized primer sequence
 <400> 15
 gaggaattca tacatgtatc cagattttaa aggaa 35
 <210> 16
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Artificially synthesized primer sequence
 <400> 16
 ggtaagcttt cattaaccgc ggcctgacctg 30
 <210> 17
 <211> 806
 <212> DNA
 <213> Bacillus subtilis
 <220>
 <221> CDS
 <222> (12)...(794)
 <400> 17
 ggaattcata c atg tat cca gat tta aaa gga aaa gtc gtc gct att aca 50
 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr
 1 5 10
 gga gct gct tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag 98
 Gly Ala Ala Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys
 15 20 25
 gag cag gca aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg 146
 Glu Gln Ala Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro
 30 35 40 45

aac gag gta aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc Asn Glu Val Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val 50 55 60	194
gtc caa gga gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa Val Gln Gly Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln 65 70 75	242
acg gca att aag gag ttc ggc aca ctc gat att atg att aat aat gcc Thr Ala Ile Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala 80 85 90	290
ggt ctt gaa aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg Gly Leu Glu Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp 95 100 105	338
gat aaa gtc atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt Asp Lys Val Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg 110 115 120 125	386
gaa gcg att aaa tat ttc gta gaa aac gat atc aag gga aat gtc att Glu Ala Ile Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile 130 135 140	434
aac atg tcc agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac Asn Met Ser Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His 145 150 155	482
tat gcg gca agt aaa ggc ggg ata aag ctg atg aca gaa aca tta gcg Tyr Ala Ala Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala 160 165 170	530
ttg gaa tac gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt Leu Glu Tyr Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly 175 180 185	578
gcg atc aac acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag Ala Ile Asn Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln 190 195 200 205	626
aaa gct gat gta gaa agc atg att cca atg gga tat atc ggc gaa ccg Lys Ala Asp Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro 210 215 220	674
gag gag atc gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc Glu Glu Ile Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser 225 230 235	722
tac gtc aca ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat Tyr Val Thr Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr 240 245 250	770
cct tca ttc cag gca ggc cgc ggt taatgaaagc tt Pro Ser Phe Gln Ala Gly Arg Gly 255 260	806

<210> 18
 <211> 261
 <212> PRT
 <213> Bacillus subtilis

<400> 18
 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1 5 10 15
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
 20 25 30
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
 35 40 45
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Gln Gly
 50 55 60
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65 70 75 80
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
 85 90 95
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
 100 105 110
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
 130 135 140
 Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
 145 150 155 160
 Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
 165 170 175
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
 180 185 190
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
 195 200 205
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
 210 215 220
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
 225 230 235 240
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
 245 250 255
 Gln Ala Gly Arg Gly
 260